



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109804

TO: Sumesh Kaushal
Location: cm1/12a07/11e12
Art Unit: 1636
December 13, 2003

Case Serial Number: 09/205658

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

* hcpm & hcpm files removed - SK

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:11 ; Search time 15.8324 Seconds
(without alignments)
2496.336 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 IIKIVSNKRRYQEDGFDL.....RREDKFNFFPQLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1362	100.0	249	21 AAB13325	Caenorhabditis ele
2	1354	99.4	383	19 AAW61534	Homo sapiens P-TEN
3	1354	99.4	394	20 AAY07457	Dog tumour suppress
4	1354	99.4	403	19 AAW64784	Human tumour suppress
5	1354	99.4	403	20 AAY07462	Mouse MMAC1 protei
6	1354	99.4	403	20 AAY07467	Dog MMAC1 protei
7	1354	99.4	403	20 AAY07468	Mouse MMAC1 protei
8	1354	99.4	403	20 AAY07451	Mouse tumour suppress
9	1354	99.4	403	20 AAY07444	Human tumour suppress

10	1354	99.4	403	20	AAW97802	Dual specificity p
11	1354	99.4	403	21	AAW80119	Human PTEN protein
12	1354	99.4	403	22	AAU08939	Human protein phos
13	1354	99.4	403	22	AAG67452	Amino acid sequenc
14	1354	99.4	403	22	AAG67631	Amino acid sequenc
15	1354	99.4	403	23	ABP65106	Hypoxia-induced pr
16	1354	99.4	403	23	AAE24851	Human phosphoinosi
17	1354	99.4	403	23	AAE17879	Human PTEN protein
18	1354	99.4	430	20	AAE17879	Dog TS10q23.3 gene
19	1354	99.4	559	20	AAE17879	Mouse TS10q23.3 ge
20	1354	99.4	559	20	AAE17879	Protein encoded by
21	1354	99.4	565	18	AAW34402	Human TS10q23.3 ge
22	1354	99.4	597	20	AAW07450	Human tumour suppress
23	1354	99.4	597	20	AAW07450	Human PTEN protein
24	1354	99.4	597	20	AAW07450	Human tumour suppress
25	1354	99.4	597	20	AAW07450	Human PTEN protein
26	1354	99.4	597	20	AAW07450	Human PTEN protein
27	1354	99.4	597	20	AAW07450	Human PTEN protein
28	1354	99.4	597	20	AAW07450	Human PTEN protein
29	1354	99.4	597	20	AAW07450	Human PTEN protein
30	1354	99.4	597	20	AAW07450	Human PTEN protein
31	1354	99.4	597	20	AAW07450	Human PTEN protein
32	1354	99.4	597	20	AAW07450	Human PTEN protein
33	1354	99.4	597	20	AAW07450	Human PTEN protein
34	1354	99.4	597	20	AAW07450	Human PTEN protein
35	1354	99.4	597	20	AAW07450	Human PTEN protein
36	1354	99.4	597	20	AAW07450	Human PTEN protein
37	1354	99.4	597	20	AAW07450	Human PTEN protein
38	1354	99.4	597	20	AAW07450	Human PTEN protein
39	1354	99.4	597	20	AAW07450	Human PTEN protein
40	1354	99.4	597	20	AAW07450	Human PTEN protein
41	1354	99.4	597	20	AAW07450	Human PTEN protein
42	1354	99.4	597	20	AAW07450	Human PTEN protein
43	1354	99.4	597	20	AAW07450	Human PTEN protein
44	1354	99.4	597	20	AAW07450	Human PTEN protein
45	1354	99.4	597	20	AAW07450	Human PTEN protein

ALIGNMENTS

RESULT 1

AAB13325
ID AAB13325 standard; Protein; 249 AA.

AC AAB13325;

XX AAB13325;

DT 12-JAN-2001 (first entry)

XX Caenorhabditis elegans DAF-18 phosphatase domain.

DE Caenorhabditis elegans; daf-18; insulin signalling pathway;

DE daf-2; age-1; insulin receptor; PI-3-kinase; PKB kinase;

DE PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes.

XX Caenorhabditis elegans.

XX WO200033068-A1.

PN 08-JUN-2000.

PD 02-DEC-1999; 99WO-US28529.

PF 03-DEC-1998; 98US-0205658.

PR (GSHO) GEN HOSPITAL CORP.

XX Ruvkun G, Ogg S;

XX WPT; 2000-423022/36.

XX Diagnosing and treating obesity and impaired glucose tolerance using

XX modulators of daf-18 expression and/or activity -

PT

XX Disclosure; Fig 398; 402pp; English.

XX The present sequence is the phosphatase domain of *Caenorhabditis elegans*

CC DAF-18 protein, which is one of a number of *C. elegans* proteins that have

CC been identified as homologues of proteins in the mammalian insulin

CC signalling pathway. The *C. elegans* age-1 gene encodes a homologue of

CC the mammalian PI 3-kinase whilst *daf-2* encodes a homologue of the

CC mammalian insulin receptor. The *C. elegans* AKT kinase and PKB kinase

CC act downstream of *daf-2* and *age-1*, just as their mammalian homologues

CC act downstream of insulin signalling. The *C. elegans* PTEN lipid

CC phosphatase homologue, DAF-18, has been found to act upstream of AKT in

CC the pathway. This discovery has enabled mammalian PTEN action to be

CC mapped to the insulin signalling pathway. Conserved DAF motifs can be

CC used to design probes to identify mammalian DAF homologues and thus to

CC identify individuals with a predisposition toward the development of

CC glucose intolerance conditions, such as obesity and diabetes.

XX

SQ Sequence 249 AA;

Query Match 100.0%; Score 1362; DB 21; Length 249;

Best Local Similarity 100.0%; Pred. No. 7.6e-147;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

DB 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

DB 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

QY 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180

DB 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240

DB 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240

QY 241 P Q L P V C G D 249

DB 241 P Q L P V C G D 249

RESULT 2

AAW61534

ID AAW61534 standard; Protein; 383 AA.

XX AAW61534;

XX

DT 09-NOV-1998 (first entry)

DE Homo sapiens P-TEN tumour suppressor.

XX

KW P-TEN; tumour suppressor; cancer; diagnosis; treatment; glioblastoma;

KW Cowden disease; melanoma; prostate; breast; brain.

XX

OS Homo sapiens.

XX

PN W09834624-A1.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US02615.

XX

PR 07-FEB-1997; 97US-0036943.

XX

PA (COLD-) COLD SPRING HARBOR LAB.

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Parsons RE, Wigler MH;

XX

DR WPI: 1998-446939/38.

DR N-PSDB; AAV45137.

XX

PT P-TEN tumour suppressor protein and DNA, for treating cancer - and

PT P-TENS with altered, truncated or deleted phosphatase domains, for

PT diagnosing and treating cancer and Cowden disease

XX

PS Claim 9; Fig 4A; 77pp; English.

XX

CC The sequence is that of the P-TEN tumour suppressor protein.

CC It can be used to diagnose cancer (glioblastoma, Cowden disease,

CC melanoma, or cancer of the prostate, breast or brain) by detecting

CC altered P-TEN sequences. Altered protein is detected based on a

CC loss of heterozygosity or a homozygous deletion at the P-TEN locus.

CC Cancer in a patient with altered P-TEN, with reduced or no phosphatase

CC activity, may be treated by introducing into the patient the wild-type

CC sequence. The protein is used to identify compounds which may be useful

CC as drugs for treating cancer, by testing the effects of P-TEN activity

CC on the compounds, or by testing the effect of the compounds on

CC expression of the gene. Such effects are inhibition, activation or

CC enhancement of enzymatic activity, preferably phosphatase activity.

XX

SQ Sequence 383 AA;

Query Match 99.4%; Score 1354; DB 19; Length 383;

Best Local Similarity 99.6%; Pred. No. 1.2e-145;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

DB 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180

DB 124 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240

DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 243

QY 241 P Q L P V C G D 249

DB 244 P Q L P V C G D 252

RESULT 3

AAV07457

ID AAV07457 standard; Protein; 394 AA.

XX AAV07457;

XX

DT 16-JUL-1999 (first entry)

DE Dog tumour suppressor protein TS10q23.3.

XX

KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;

KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;

KW enzyme linked immunosorbant assay; gene expression; dog.

XX

OS Canis familiaris.

XX

PN W09910537-A1.

XX

PD 04-MAR-1999.

XX

PF 26-AUG-1998; 98WO-US17636.

XX

PR 30-APR-1998; 98US-0083563.

PR 26-AUG-1997; 97US-0057750.

XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX
XX WPI; 1999-190638/16.
DR N-PSDB; AAX57673.
XX
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PT Syndrome and susceptibility to breast cancer
XX
XX Disclosure; Fig 9; 244bp; English.
XX
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX
SQ Sequence 394 AA;

Query Match 99.4%; Score 1354; DB 20; Length 394;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C L K V K I Y S S N S G P T R E D K F N Y P E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C L K V K I Y S S N S G P T R E D K F N Y P E F 243

QY 241 P Q L P V C G D 249
DB 244 P Q L P V C G D 252

RESULT 4
AAW64784
ID AAW64784 standard; Protein; 403 AA.
XX
AC AAW64784;
XX
DT 03-NOV-1998 (first entry)
XX
DE Human tumour suppressor TS10q23.3 protein.
XX
XX Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;
KW brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;
KW drug screening.
XX
XX Homo sapiens.
OS
XX WO9833907-A1.
XX
XX 06-AUG-1998.
PD
XX 08-JAN-1998; 98WO-US00353.
PF
XX

PR 30-JAN-1997; 97US-0791115.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX
XX WPI; 1998-437461/37.
DR N-PSDB; AAV46392..
XX
XX Tumour suppressor TS10q23.3 and related antibodies - useful for
PT diagnosis, staging and treatment of cancer, especially of breast,
PT prostate and brain
XX
XX Claim 1; Fig 7; 161pp; English.
PS
XX This sequence represents the human tumour suppressor protein TS10q23.3.
CC This protein can be used to diagnose a wide range of tumours,
CC particularly of prostate, breast and brain (glioma), to stage cancers
CC (particularly differentiation between low grade brain cancer and glioma)
CC and for prediction of metastasis. This suppressor and its nucleic acid
CC are also used to alter the phenotype to specifically treat cancer cells,
CC e.g. by in vivo or ex vivo gene therapy, optionally together with other
CC anti-cancer agents. Fragments of the suppressor can be coupled to an
CC immunogenic carrier and are used to raise antibodies, to isolate
CC antigens, as immunoassay reagents, to clone related DNA or for
CC immunotherapy. Antisense nucleic acid can be used to produce transgenic
CC animals (useful for drug screening) or to eliminate dominant negative
CC mutants.
XX
SQ Sequence 403 AA;

Query Match 99.4%; Score 1354; DB 19; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C L K V K I Y S S N S G P T R E D K F N Y P E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C L K V K I Y S S N S G P T R E D K F N Y P E F 243

QY 241 P Q L P V C G D 249
DB 244 P Q L P V C G D 252

RESULT 5
AAV07462
ID AAV07462 standard; peptide; 403 AA.
XX
AC AAV07462;
XX
DT 16-JUL-1999 (first entry)
XX
DE Mouse MMAC1 protein sequence.
XX
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW enzyme linked immunosorbant assay; gene expression; mouse.
XX
XX Mus musculus.
OS

XX WO9910537-AL.
 PN 04-MAR-1999.
 PD 26-AUG-1998; 98WO-US17636.
 PF 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 PI WPI; 1999-190638/16.
 DR Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Disclosure; Page 226-227; 244pp; English.
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3.
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX Sequence 403 AA;
 SQ Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
 Db 124 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 6
 AAY07467
 ID AAY07467 standard; Protein; 403 AA.
 XX AAY07467;
 XX 16-JUL-1999 (first entry)
 DT Dog MMAC1 protein.
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; dog.
 XX

OS Canis familiaris.
 XX WO9910537-AL.
 PN 04-MAR-1999.
 PD 26-AUG-1998; 98WO-US17636.
 PF 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 PI WPI; 1999-190638/16.
 DR N-PSDB; AAX57699.
 DR Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Claim 3; Page 232-233; 244pp; English.
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3.
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX Sequence 403 AA;
 SQ Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
 Db 124 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 7
 AAY07468
 ID AAY07468 standard; Protein; 403 AA.
 XX AAY07468;
 XX 16-JUL-1999 (first entry)
 DT Mouse MMAC1 protein.
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; dog.

enzyme linked immunosorbant assay; gene expression; mouse.

Mus musculus.
WO9910537-A1.
04-MAR-1999.
26-AUG-1998; 98WO-US17636.
30-APR-1998; 98US-0083563.
26-AUG-1997; 97US-0057750.
(MYRI-) MYRIAD GENETICS INC.
(TEXA) UNIV TEXAS SYSTEM.
Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
Yung WKA;
WPI; 1999-190638/16.
N-PSDB; AAX57700.
Newly isolated DNA or RNA polynucleotide encoding a mutant tumour suppressor (TS10q23.3) - useful for the diagnosis of Cowden's Syndrome and susceptibility to breast cancer
Disclosure; Page 236-238; 244pp; English.
The invention relates to mutant genes encoding the tumour suppressor TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of Cowden's Syndrome in cells selected from the breast, ovaries, thyroid gland and endometrium (claimed). The mutant gene is also useful for diagnosing a subject who has a predisposition to breast cancer. Both methods involve antibodies, which specifically bind to a TS10q23.3, used in an ELISA assay to evaluate the level of TS10q23.3 expression.

Query Match 99.4%; Score 1354; DB 20; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S N K R R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
DB 4 I I K E I V S N K R R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y P E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y P E F 243
QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 8
AAV07451
ID AAY07451 standard; Protein; 403 AA.
AC AAY07451;
XX
DT 16-JUL-1999 (first entry)
XX
DE Mouse tumour suppressor protein TS10q23.3.
XX

Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary; Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA; enzyme linked immunosorbant assay; gene expression; mouse.
Mus musculus.
WO9910537-A1.
04-MAR-1999.
26-AUG-1998; 98WO-US17636.
30-APR-1998; 98US-0083563.
26-AUG-1997; 97US-0057750.
(MYRI-) MYRIAD GENETICS INC.
(TEXA) UNIV TEXAS SYSTEM.
Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
Yung WKA;
WPI; 1999-190638/16.
N-PSDB; AAX57672.
Newly isolated DNA or RNA polynucleotide encoding a mutant tumour suppressor (TS10q23.3) - useful for the diagnosis of Cowden's Syndrome and susceptibility to breast cancer
Disclosure; Fig 9; 244pp; English.
The invention relates to mutant genes encoding the tumour suppressor TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of Cowden's Syndrome in cells selected from the breast, ovaries, thyroid gland and endometrium (claimed). The mutant gene is also useful for diagnosing a subject who has a predisposition to breast cancer. Both methods involve antibodies, which specifically bind to a TS10q23.3, used in an ELISA assay to evaluate the level of TS10q23.3 expression.

Query Match 99.4%; Score 1354; DB 20; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S N K R R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
DB 4 I I K E I V S N K R R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y P E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y P E F 243
QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 9
AAV07444
ID AAY07444 standard; Protein; 403 AA.
AC AAY07444;
XX
DT 16-JUL-1999 (first entry)
XX

DE Human tumour suppressor protein TS10q23.3.
 XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; human.
 XX Homo sapiens.
 OS
 XX WO9910537-A1.
 PN
 XX
 XX
 XX 04-MAR-1999.
 PD
 XX
 XX 26-AUG-1998; 98WO-US17636.
 PF
 XX
 XX 30-APR-1998; 98US-0083563.
 PR
 XX 26-AUG-1997; 97US-0057750.
 PR
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 PI
 XX WPI: 1999-190638/16.
 DR N-PSDB; AAX57671.
 DR
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 PT
 XX Disclosure; Fig 7; 244pp; English.
 PS
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX
 SQ Sequence 403 AA;
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S Q R R Y Y Y Y S Y L L K 180
 Db 124 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S Q R R Y Y Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W Q L K V I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W Q L K V I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 10
 AAW97802
 ID AAW97802 standard; Protein; 403 AA.
 XX
 AC AAW97802;
 XX

DT 21-MAY-1999 (first entry)
 XX Dual specificity phosphatase PTEN.
 DE
 XX PTEN; MMAC1; protein tyrosine phosphatase; human; prostate cancer;
 KW brain cancer; prostate cancer; tumour suppressor; Cowden's disease;
 KW neurodegenerative disease; Parkinson's disease; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX WO9902704-A2.
 PN
 XX
 XX 21-JAN-1999.
 PD
 XX
 XX 08-JUL-1998; 98WO-US14205.
 PF
 XX
 XX 29-JUN-1998; 98US-0090984.
 PR
 XX 08-JUL-1997; 97US-0051908.
 PR
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 XX Myers MP, Tonks NK;
 PI WPI: 1999-120905/10.
 DR N-PSDB; AAX07339.
 DR
 XX New use of PTEN phosphatase - for developing products for the
 PT diagnosis and treatment of hyperproliferative disorders, e.g.
 PT cancers or neurodegenerative disorders such as Parkinson's disease
 PT
 XX Disclosure; Fig 1A-C; 60pp; English.
 PS
 XX This is the amino acid sequence of human PTEN phosphatase,
 CC predicted from the PTEN gene (see AAX07339) located at 10q22-23.
 CC PTEN shares homology with the protein tyrosine phosphatase
 CC family. It can function as a dual specificity phosphatase in
 CC vitro, displaying selectivity for extremely acidic substrates.
 CC PTEN dephosphorylates phosphatidylinositol in vitro, and displays
 CC selectivity for the 3 position of the inositol ring. It is also
 CC able to dephosphorylate serine, threonine and tyrosine residues
 CC when present in acidic substrates. The phosphatase activity of
 CC PTEN is required for its ability to function as a tumour suppressor
 CC or an apoptosis inducer. Point mutations, including point mutations
 CC in tumour samples and Cowden's disease kindreds, ablate PTEN
 CC activity. PTEN functions as an upstream, negative regulator of
 CC PKB/Akt and has the potential to regulate signals associated with
 CC control of cell survival. PTEN polypeptides and polynucleotides
 CC can be used in the diagnosis and treatment of conditions
 CC characterised by an alteration in PTEN which causes an alteration
 CC of phosphatase activity. They can be used to treat
 CC hyperproliferative conditions such as cancers, e.g. brain, prostate
 CC or breast cancers or Cowden's disease, or other hyperproliferative
 CC diseases involving reduced phosphatase activity. They can also be
 CC used in methods of reducing PTEN phosphatase activity for treating
 CC conditions such as Parkinson's disease and other neurodegenerative
 CC disease.
 XX
 SQ Sequence 403 AA;
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S Q R R Y Y Y Y S Y L L K 180
 Db 124 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S Q R R Y Y Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W Q L K V I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W Q L K V I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252

Db 124 CKAKGRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPSQRRVYVYYSYLLK 183
Qy 181 NHDYRPVALLFHQMFTIPMFSGGTCNPQFVVCQKVKIYSSNSGTRREDKFNYPEF 240
Db 184 NHDYRPVALLFHQMFTIPMFSGGTCNPQFVVCQKVKIYSSNSGTRREDKFNYPEF 243
Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 11
ID AAY80119 standard; Protein; 403 AA.
XX AC AAY80119;
DT 22-MAY-2000 (first entry)
XX DE Human PTEN protein sequence SEQ ID NO:1.
XX KW Human; PTEN; MMAC1; TEPI; phosphothioate; antisense oligonucleotide;
KW inhibition; protein phosphatase; tumour; diagnosis; inflammation;
KW anticancer; anti-inflammatory; anti-infective; infection.
XX OS Homo sapiens.
XX FN US6020199-A.
XX PD 01-FEB-2000.
XX PF 21-JUL-1999; 99US-0358381.
XX PR 21-JUL-1999; 99US-0358381.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowsert LM;
XX DR WPI; 2000-181363/16.
XX DR N-PSDB; AAZ91361.
XX PT New antisense compounds useful for treating, preventing or diagnosing
PT e.g. tumors or inflammation, are targeted to the human dual specificity
PT protein phosphatase (PTEN) sequence -
XX PS Claim 1; Column 43-46; 32pp; English.
XX CC The present invention describes phosphorothioate antisense
CC oligonucleotides that are targeted to the 3'-untranslated region (UTR)
CC of the sequence encoding a human dual specificity protein phosphatase
CC designated PTEN (also known as MMAC1 and TEPI), and hybridise
CC specifically to the human PTEN nucleotide sequence given in AAZ91361.
CC The antisense oligonucleotides have anticancer, anti-inflammatory and
CC anti-infective activities. The phosphorothioate antisense
CC oligonucleotides can be used for diagnosis, treatment and prevention of
CC PTEN-related diseases, e.g. infections, inflammation and tumours.
CC The present sequence represents the human PTEN protein sequence.
XX SQ Sequence 403 AA;

Query Match 99.4%; Score 1354; DB 21; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 60
Db 4 I I K E I V S N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 63
Qy 61 H Y K I N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
Db 64 H Y K I N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 123

Qy 121 CKAKGRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPSQRRVYVYYSYLLK 180
Db 124 CKAKGRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPSQRRVYVYYSYLLK 183
Qy 181 NHDYRPVALLFHQMFTIPMFSGGTCNPQFVVCQKVKIYSSNSGTRREDKFNYPEF 240
Db 184 NHDYRPVALLFHQMFTIPMFSGGTCNPQFVVCQKVKIYSSNSGTRREDKFNYPEF 243
Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 12
ID AAU08939 standard; Protein; 403 AA.
XX AC AAU08939;
DT 18-DEC-2001 (first entry)
XX DE Human protein phosphatase PTEN.
XX KW Human; PTEN; MMAC1; TEPI; protein phosphatase; antisense;
KW antiinflammatory; cytostatic; antidiabetic; antilipaeamic;
KW infection; inflammation; tumour; diabetes; insulin resistance;
KW insulin sensitivity; triglyceride control; cholesterol control.
XX OS Homo sapiens.
XX FN US6284538-B1.
XX PD 04-SEP-2001.
XX PF 24-MAY-2000; 2000US-0577902.
XX PR 21-JUL-1999; 99US-0358381.
XX PR 14-DEC-1999; 99WO-US29594.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowsert LM, McKay R;
XX DR WPI; 2001-588976/66.
XX DR N-PSDB; AAS13987.
XX PT New antisense oligonucleotides targeting nucleic acids encoding PTEN,
PT useful for treating diabetes, increasing insulin sensitivity, or
PT decreasing insulin resistance, blood triglyceride or cholesterol levels
PT in a diabetic animal -
XX PS Example 13; Column 53-55; 38pp; English.
XX CC The invention relates to a compound targeted to a nucleic acid encoding
CC PTEN (a dual specificity protein phosphatase), where the compound is an
CC antisense oligonucleotide. The antisense oligonucleotides are useful in
CC modulating the function of nucleic acids encoding PTEN, ultimately
CC modulating the amount of PTEN produced. The antisense compounds can be used
CC as diagnostics, therapeutics, prophylactics (e.g. to prevent or delay
CC infection, inflammation or tumour formation), and as research agents and
CC kits. The antisense compounds are also useful in treating diabetes,
CC decreasing insulin resistance, increasing insulin sensitivity and
CC decreasing blood triglyceride or cholesterol levels in a diabetic animal.
CC The present sequence is human PTEN (also known as MMAC1/TEPI).
XX SQ Sequence 403 AA;

Query Match 99.4%; Score 1354; DB 22; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 60
Db 4 I I K E I V S N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 63
Qy 61 H Y K I N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
Db 64 H Y K I N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 123

Db 4 I I K I E V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
 Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 243
 QY 241 P Q L P V C G D 249
 Db 244 P Q L P V C G D 252

RESULT 13
 AAG67452
 ID AAG67452 standard; Protein; 403 AA.

XX AC AAG67452;
 DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of a human polypeptide.
 XX KW Human; protein kinase; protein phosphatase; signal transduction;
 XX KW intracellular signalling pathway.
 XX OS Homo sapiens.
 XX PN WO200109345-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-JP05060.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 18-OCT-1999; 99US-0159590.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 17-FEB-2000; 2000US-0183322.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 XX PI Senoo C, Nezu J;
 XX WPI; 2001-564736/63.
 XX PT New genes encoding protein kinase and protein phosphatase, useful for
 XX PT identifying modulators which can be used to treat human or animal
 XX PT disorders associated with the expression or function of these enzymes -
 XX PS Example 4; Page 288-291; 336pp; Japanese.
 XX CC The specification describes human protein kinase/protein phosphatases.
 XX CC The polypeptides are expected to participate in signal transduction
 XX CC in cells. The kinase phosphatases are connected with intracellular
 XX CC signalling pathways. Antisense oligonucleotides and compounds
 XX CC identified by screening (agonists or antagonists) can be used to
 XX CC treat human or animal disorders associated with the expression
 XX CC or function of the protein. In addition, the polypeptides may be used
 XX CC as target molecules for drug development. The present sequence
 XX CC represents a polypeptide, used in the course of the invention.
 XX SQ Sequence 403 AA;
 Query Match 99.4%; Score 1354; DB 22; Length 403;

Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K I E V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K I E V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
 Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 243
 QY 241 P Q L P V C G D 249
 Db 244 P Q L P V C G D 252

RESULT 14
 AAG67631
 ID AAG67631 standard; Protein; 403 AA.

XX AC AAG67631;
 DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of a human protein.
 XX KW Human; protein kinase; protein phosphatase; signal transduction.
 XX OS Homo sapiens.
 XX PN WO200109316-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-JP05061.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 18-OCT-1999; 99US-0159590.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 17-FEB-2000; 2000US-0183322.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PR 09-JUN-2000; 2000JP-0241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 XX PI Senoo C, Nezu J;
 XX WPI; 2001-570286/64.
 XX PT New genes encoding proteins with protein kinase/protein phosphatase
 XX PT activity, useful in the diagnosis and treatment of diseases -
 XX PS Example 4; Page 188-191; 233pp; Japanese.
 XX CC The specification describes human protein kinase/protein phosphatases.
 XX CC It is expected that the protein kinase/protein phosphatase gene
 XX CC participates in signal transduction in cells. The protein
 XX CC kinase/protein phosphatase polypeptides and polynucleotides are
 XX CC useful for developing diagnostics and treatment agents for human
 XX CC and animal diseases. The protein kinase/protein phosphatase polypeptides
 XX CC are useful as target molecules in designing novel drugs. The protein
 XX CC kinase/protein phosphatase polynucleotides are useful as a source of
 XX CC probes and primers, which may be used to isolate homologous sequences.

CC The present sequence represents a human protein, which is used in the
CC course of the invention.

SQ	Sequence	403 AA;
	Query Match	99.4%; Score 1354; DB 22; Length 403;
	Best Local Similarity	99.6%; Pred. No. 1.2e-145;
	Matches 248; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1	I I K E I V S R N K R R Y Q O D G F D L D T I Y P N I I T A M G P P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db	4	I I K E I V S R N K R R Y Q O D G F D L D T I Y P N I I T A M G P P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
QY	61	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P P O L E L I K P C E D L D W L S E D D N H V A A I H 120
Db	64	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P P O L E L I K P C E D L D W L S E D D N H V A A I H 123
QY	121	C K A G K G R T G W M I C A Y L L H R G K F L K A Q A L D F Y G E V R T R D K K G V T I P S O R R V V Y Y S Y L L K 180
Db	124	C K A G K G R T G W M I C A Y L L H R G K F L K A Q A L D F Y G E V R T R D K K G V T I P S O R R V V Y Y S Y L L K 183
QY	181	N H L D Y R P V A L L F H K W M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
Db	184	N H L D Y R P V A L L F H K W M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY	241	P Q P L P V C G D 249
Db	244	P Q P L P V C G D 252

RESULT 15

ABP65106	
ID	ABP65106 standard; Protein; 403 AA.
XX	
XX	
AC	ABP65106;
XX	
DT	12-NOV-2002 (first entry)
XX	
DE	Hypoxia-induced protein #32.
XX	
KW	Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW	antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
KW	hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
KW	ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW	preclampsia; atherosclerosis; inflammatory condition; wound healing;
KW	inflammation; erythropoiesis; hair loss; human.

OS Homo sapiens.

PN WO200246465-A2.

T3-JUN-2002.

10-DEC-2001:

08-DEC-2000. 2000GB-0030076

PR 08-FEB-2001; 2001GB-0003156.
PB 25-OCT-2001; 2001GB-0025666

XX
PA
(OYEO-) OYEOB BIOMERICA IV

XX		White	Minder	Wood	Ward	Cover	Village	CM	Threat	D
----	--	-------	--------	------	------	-------	---------	----	--------	---

PI Rayner WN;
....

DR WPI; 2002-627238/67.

PT Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene -

PS Claim 13; Page 310; 538pp; English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABH6561-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

Sequence 403 AA;

Query Match	99.4%;	Score 1354;	DB 23;	Length 403;
Best Local Similarity	99.6%;	Pred. No. 1.2e-145;		
Matches 248;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	IIKEIVSNKRRYQBDGDFDLDTIYYPNI	IAMGFPAERLEGVYRNNDIVVRF	FLDSKHKN 60
DB	4	IIKEIVSNKRRYQBDGDFDLDTIYYPNI	IAMGFPAERLEGVYRNNDIVVRF	FLDSKHKN 63
QY	61	HYKIYNLCAERHYDTAKENCVAQYPP	EDHNPQLELIKPCEDLDQWLS	EDDNHVAIHH 120
DB	64	HYKIYNLCAERHYDTAKENCVAQYPP	EDHNPQLELIKPCEDLDQWLS	EDDNHVAIHH 123
QY	121	CKAGKRGTVMICAYLLHRGFLKAQEA	LDIFYGEVTRDKKGVTPSQRRRYV	YYYSYLLK 180
DB	124	CKAGKRGTVMICAYLLHRGFLKAQEA	LDIFYGEVTRDKKGVTPSQRRRYV	YYYSYLLK 183
QY	181	NHLDYRPVALLFHKMMFETIIPW	SGGTGNPQVVCQVKIYSSNSG	PTREDKFNPEEF 240
DB	184	NHLDYRPVALLFHKMMFETIIPW	SGGTGNPQVVCQVKIYSSNSG	PTREDKFNPEEF 243
QY	241	POPLPVCGD	249	
DB	244	POPLPVCGD	252	

Search completed: December 10, 2003, 20:32:15
Job time : 16.8324 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:47 ; Search time 6.16846 Seconds
(without alignments)
1707.948 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 IIKIVSNKRYQEDGFDL.....RDEKFNFFPQLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42110858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1354	99.4	394	3	US-08-791-115B-27
2	1354	99.4	394	4	US-09-140-749-17
3	1354	99.4	403	3	US-08-791-115B-1
4	1354	99.4	403	3	US-08-791-115B-23
5	1354	99.4	403	3	US-08-791-115B-25
6	1354	99.4	403	4	US-09-140-749-2
7	1354	99.4	403	4	US-09-140-749-10
8	1354	99.4	403	4	US-09-140-749-49
9	1354	99.4	403	4	US-09-140-749-55
10	1354	99.4	403	4	US-09-140-749-57
11	1354	99.4	430	3	US-08-791-115B-7
12	1354	99.4	430	4	US-09-140-749-18
13	1354	99.4	559	4	US-09-140-749-15
14	1354	99.4	565	3	US-08-906-156A-12
15	1354	99.4	597	4	US-09-140-749-8
16	1354	99.4	645	3	US-08-791-115B-5
17	1354	99.4	742	3	US-08-791-115B-6
18	294	21.6	60	3	US-08-791-115B-20
19	294	21.6	60	4	US-09-140-749-31
20	287	21.1	60	3	US-08-791-115B-19
21	287	21.1	60	4	US-09-140-749-30
22	286	21.0	60	3	US-08-791-115B-21
23	286	21.0	60	4	US-09-140-749-32
24	121.5	8.9	170	3	US-08-725-532A-1
25	121.5	8.9	173	3	US-08-725-532A-6
26	121.5	8.9	173	4	US-09-164-193-20
27	121.5	8.9	173	4	US-09-221-448A-20

28	120	8.8	278	3	US-08-821-278A-18	Sequence 18, Appl
29	120	8.8	802	3	US-09-081-345-18	Sequence 18, Appl
30	113	8.3	594	4	US-09-468-872-2	Sequence 2, Appl
31	112.5	8.3	167	3	US-08-725-532A-5	Sequence 5, Appl
32	109	8.0	173	3	US-08-725-532A-3	Sequence 3, Appl
33	109	8.0	173	3	US-09-164-193-2	Sequence 2, Appl
34	109	8.0	173	4	US-08-221-448A-2	Sequence 2, Appl
35	107	7.9	22	3	US-08-906-156A-76	Sequence 76, Appl
36	102.5	7.5	807	3	US-09-081-345-2	Sequence 2, Appl
37	102	7.5	289	1	US-08-036-210-13	Sequence 13, Appl
38	102	7.5	289	2	US-08-449-609-13	Sequence 13, Appl
39	102	7.5	289	4	US-09-361-096A-13	Sequence 13, Appl
40	101	7.4	250	2	US-08-685-932-7	Sequence 7, Appl
41	101	7.4	250	2	US-09-144-925-7	Sequence 7, Appl
42	99	7.3	277	2	US-08-685-932-22	Sequence 22, Appl
43	99	7.3	277	2	US-09-144-925-22	Sequence 22, Appl
44	98.5	7.2	116	1	US-07-988-273-5	Sequence 5, Appl
45	98.5	7.2	116	5	PCT-US93-12019-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-791-115B-27
; Sequence 27, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08791.115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-115B-27

Query Match 99.4%; Score 1354; DB 3; Length 394;
Best Local Similarity 99.6%; Pred. No. 2.2e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIKIVSNKRYQEDGFDLDTIYPNIIAMGPPAERLEGVYRNNDVVRFDLSKHN 60

DB 4 IIKIVSNKRYQEDGFDLDTIYPNIIAMGPPAERLEGVYRNNDVVRFDLSKHN 63

QY 61 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 120
Db 64 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 123
QY 121 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 180
Db 124 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 183
QY 181 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 240
Db 184 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 243
QY 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 2

US-09-140-749-17
; Sequence 17, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-17

Query Match 99.4%; Score 1354; DB 4; Length 394;
Best Local Similarity 99.6%; Pred. No. 2.2e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 120
Db 64 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 123
QY 121 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 180
Db 124 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 183
QY 181 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 240
Db 184 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 243
QY 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 3

US-08-791-115B-1

; Sequence 1, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-1

Query Match 99.4%; Score 1354; DB 3; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 120
Db 64 HYKYNLCARHYDTAKNCRVAQYPPEDHNPQLELIKPFCELDQWLSEDDNHVAI 123
QY 121 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 180
Db 124 CKAGKRTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 183
QY 181 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 240
Db 184 NHLDRPVALLFHKMFETIPMFSGGTGNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 243
QY 241 POPLPVCGD 249
Db 244 POPLPVCGD 252
RESULT 4
US-08-791-115B-23
; Sequence 23, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.

APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
TELEPHONE: 202-683-6040
TELEFAX: 202-683-7031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-115B-23

Query Match 99.4%; Score 1354; DB 3; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 I I K E I V S N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 60
Db 4 I I K E I V S N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 63
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 243
Qy 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 5
US-08-791-115B-25
Sequence 25, Application US/08791115B
Patent No. 6262242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
TELEPHONE: 202-683-6040
TELEFAX: 202-683-7031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-115B-25

Query Match 99.4%; Score 1354; DB 3; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 I I K E I V S N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 60
Db 4 I I K E I V S N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 63
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 243
Qy 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 6
US-09-140-749-2
Sequence 2, Application US/09140749
Patent No. 6482795
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, Alfred W.K.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
FILE REFERENCE: 2318-205
CURRENT APPLICATION NUMBER: US/09/140,749
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: U.S. 08/791,115
EARLIER FILING DATE: 1997-01-30
EARLIER APPLICATION NUMBER: U.S. 60/057,750

; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-749-2

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 8
US-09-140-749-49
; Sequence 49, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-49

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 9
US-09-140-749-55
; Sequence 55, Application US/09140749
; Patent No. 6482795

; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-749-2

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 7
US-09-140-749-10
; Sequence 10, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-10

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120

```
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-55

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K E N Y F E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K E N Y F E F 243

QY 241 P Q P L P V C G D 249
Db 244 P Q P L P V C G D 252

RESULT 10
US-09-140-749-57
; Sequence 57, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 403

; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 403

; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/08/791,115B
; CURRENT FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-7

Query Match 99.4%; Score 1354; DB 3; Length 430;
```

[illegible]

```

RESULT 12
US-09-140-749-18
; Sequence 18, Application US/09140749
; Patent No. 6483795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-18

```

Query Match	99.4%;	Score 1354;	DB 4;	Length 430;
Best Local Similarity	99.6%;	Pred. No. 2.5e-142;		
Matches 248;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	IIKEIYSRNKRRVQEDGFDLDTIYFNIIAMGFPAAERLEGVYRNNDVVVFLDLSKHKN	60	
DB	40	IIKEIYSRNKRRVQEDGFDLDTIYFNIIAMGFPAAERLEGVYRNNDVVVFLDLSKHKN	99	
QY	61	HYKIYNLCABRHVDYTAQFNCRVAQYPEDHNPPQLELIKPCEDLDQWLSEDDNNHVAIHH	120	
DB	100	HYKIYNLCABRHVDYTAQFNCRVAQYPEDHNPPQLELIKPCEDLDQWLSEDDNNHVAIHH	159	
QY	121	CKAGKGRGVMICYALLHRGKFLKAQALDPYGEVRTDKKGVTPSORRVVYVYSYLLK	180	
DB	160	CKAGKGRGVMICYALLHRGKFLKAQALDPYGEVRTDKKGVTPSORRVVYVYSYLLK	219	
QY	181	NHLDYRPVALLFHKKMFETTPMFSGGTCNPOFVVCQLKVKIYSNSGPTREDFKNPFEP	240	
DB	220	NHLDYRPVALLFHKKMFETTPMFSGGTCNPOFVVCQLKVKIYSNSGPTREDFKNPFEP	279	
QY	241	ROELPVCVD	249	

```

Db      280 PQPLPVCGD 288          |||||
                                           |||||
RESULT 13
US-09-140-749-15
; Sequence 15, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS1Q023.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: patentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-15

```

RESULT 14
US-08-906-156A-12
; Sequence 12, Application US/08906156A
; Patent No. 6287854
; GENERAL INFORMATION:
; APPLICANT: SPURR, NIGEL K
; APPLICANT: GRAY, IAN C
; APPLICANT: STEWART, LORNA M
; TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
; TITLE OF INVENTION: AND TREATMENT THEREOF
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA

COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,156A
FILING DATE: 05-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,655
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,147
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,840
FILING DATE: 23-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/96GB/02588
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1090-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Translation of partial cDNA sequence
US-08-906-156A-12

Query Match 99.4%; Score 1354; DB 3; Length 565;
Best Local Similarity 99.6%; Pred. No. 3.7e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db 166 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 225

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 226 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 285

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 286 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 345

Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K F N Y F E F 240
Db 346 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K F N Y F E F 405

Qy 241 P Q P L P V C G D 249
Db 406 P Q P L P V C G D 414

RESULT 15
US-09-140-749-8
; Sequence 8, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter

APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, Alfred W.K.
APPLICANT: Tavtigan, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
FILE REFERENCE: 2318-205
CURRENT APPLICATION NUMBER: US/09/140,749
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: U.S. 08/791,115
EARLIER FILING DATE: 1997-01-30
EARLIER APPLICATION NUMBER: U.S. 60/057,750
EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: U.S. 60/083,563
EARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 597
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-749-8

Query Match 99.4%; Score 1354; DB 4; Length 597;
Best Local Similarity 99.6%; Pred. No. 4e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db 198 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 257

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 258 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 317

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 318 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 377

Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K F N Y F E F 240
Db 378 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R R E D K F N Y F E F 437

Qy 241 P Q P L P V C G D 249
Db 438 P Q P L P V C G D 446

Search completed: December 10, 2003, 20:35:42
Job time : 7.16846 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model.

Run on: December 10, 2003, 20:34:18 ; Search time 11.1032 Seconds
(without alignments)
4170.856 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 I I K E I V S R K R Y Q E D G F L R E D K F N Y F P P Q L P V C G D 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	249	9	US-09-205-658-309
2	1362	100.0	249	12	Sequence 309, Appl
3	1354	99.4	394	12	Sequence 17, Appl
4	1354	99.4	403	10	US-10-299-003-17
5	1354	99.4	403	12	US-09-870-379-2
6	1354	99.4	403	12	US-10-299-003-2
7	1354	99.4	403	12	US-10-299-003-10
8	1354	99.4	403	12	US-10-299-003-49
9	1354	99.4	403	12	US-10-299-003-55
10	1354	99.4	403	12	US-10-299-003-57
11	1354	99.4	403	15	US-10-059-585-50
12	1354	99.4	430	12	US-10-299-003-18
13	1354	99.4	559	12	US-10-299-003-15
14	511	37.5	445	12	US-10-299-003-8
15	494	36.3	645	12	US-10-120-801-101

16	494	36.3	664	12	US-10-120-801-100
17	478	35.1	551	12	US-10-120-801-97
18	478	35.1	551	15	US-10-059-585-57
19	477.5	35.1	551	12	US-10-120-801-98
20	465	34.1	962	9	US-09-205-658-310
21	465	34.1	962	12	US-09-963-693-310
22	453	33.3	248	9	US-09-205-658-308
23	453	33.3	248	12	US-09-963-693-308
24	453	33.3	477	12	US-10-120-801-30
25	439	32.2	85	9	US-09-864-761-37705
26	439	32.2	86	12	US-10-029-386-30662
27	301.5	22.1	382	12	US-10-327-414-4
28	301.5	22.1	1386	12	US-10-327-414-2
29	294	21.6	60	12	US-10-299-003-31
30	287	21.1	60	12	US-10-299-003-30
31	286	21.0	60	12	US-10-299-003-32
32	285	20.9	1300	12	US-10-102-549-2
33	285	20.9	1311	12	US-10-354-358-68
34	128.5	9.4	543	12	US-10-032-585-7649
35	126	9.3	447	15	US-10-059-585-51
36	122.5	9.0	175	9	US-09-925-297-613
37	120	8.8	802	10	US-09-822-295-18
38	120	8.8	802	12	US-10-366-547-95
39	113	8.3	383	12	US-10-366-547-55
40	113	8.3	594	12	US-10-366-547-51
41	113	8.3	623	12	US-10-366-547-53
42	112.5	8.3	167	15	US-10-177-293-385
43	112	8.2	459	12	US-10-366-547-61
44	112	8.2	471	12	US-10-366-547-59
45	112	8.2	498	12	US-10-366-547-57

ALIGNMENTS

RESULT 1

US-09-205-658-309
; Sequence 309, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-309

Query Match 100.0%; Score 1362; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-134;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	I I K E I V S R K R Y Q E D G F L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N	60
Db	1	I I K E I V S R K R Y Q E D G F L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N	60
QY	61	H Y K I Y N L C A E R H Y T A K F N C V A Q P P E D H N P P Q L I K P F C E D L D Q W L S E D D H N V A I H	120
Db	61	H Y K I Y N L C A E R H Y T A K F N C V A Q P P E D H N P P Q L I K P F C E D L D Q W L S E D D H N V A I H	120

QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 180
DB 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 180
QY 181 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 240
DB 181 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 240
QY 241 POPLPVCGD 249
DB 241 POPLPVCGD 249

RESULT 2

US-09-963-693-309
; Sequence 309, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-309

Query Match 100.0%; Score 1362; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-134;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKEIVSRNKRKYQEDGFDLDTIYIPNIIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
DB 1 IIKEIVSRNKRKYQEDGFDLDTIYIPNIIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
QY 61 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
DB 61 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 180
DB 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 180
QY 181 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 240
DB 181 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 240
QY 241 POPLPVCGD 249
DB 241 POPLPVCGD 249

RESULT 3

US-10-299-003-17
; Sequence 17, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jaaser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-17

Query Match 99.4%; Score 1354; DB 12; Length 394;
Best Local Similarity 99.6%; Pred. No. 1.4e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIKEIVSRNKRKYQEDGFDLDTIYIPNIIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
DB 4 IIKEIVSRNKRKYQEDGFDLDTIYIPNIIAMGPPAERLEGVYRNNDVVRFLDSKHN 63
QY 61 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
DB 64 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPPOLELIKPFCELDQWLSDDNHVAIH 123
QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 180
DB 124 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSLLK 183
QY 181 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 240
DB 184 NHDYRPVALLPHKMFETIPMFSGGTGTCNPFVVCQKVKIYSSNGSPTRREDKFNYPEF 243
QY 241 POPLPVCGD 249
DB 244 POPLPVCGD 252

RESULT 4

US-09-870-379-2
; Sequence 2, Application US/09870379
; Patent No. US20020150954A1
; GENERAL INFORMATION:
; APPLICANT: Donald L. Durden
; APPLICANT: ADVANCED RESEARCH & TECHNOLOGY INSTITUTE
; TITLE OF INVENTION: Compositions and Methods for Identifying
; FILE REFERENCE: ARTI 0024-US
; CURRENT APPLICATION NUMBER: US/09/870,379
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17358
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/274/167
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/208,437
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-379-2

```
Query Match          99.4%; Score 1354; DB 10; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 5
US-10-299-003-2
; Sequence 2, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-2

Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 240
; Sequence 2, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-2
```

```
Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 7
US-10-299-003-49
; Sequence 49, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-10

Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252
```

```

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-49

```

```

Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183

Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243

Qy 241 P Q P L P V C G D 249
Db 244 P Q P L P V C G D 252

```

RESULT 8

```

US-10-299-003-55
; Sequence 55, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Canis familiaris

```

US-10-299-003-55

```

Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183

Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243

Qy 241 P Q P L P V C G D 249
Db 244 P Q P L P V C G D 252

```

RESULT 9

```

US-10-299-003-57
; Sequence 57, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-57

```

```

Query Match          99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y O E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D P Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183

```

Qy 181 NHDYRPVALLPHKMFETIPMFSGTCNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 240
Db 184 NHDYRPVALLPHKMFETIPMFSGTCNPQVVCOLKVKIYSSNSGPTREDKFNYPEF 243
Qy 241 POPLPVC GD 249
Db 244 POPLPVC GD 252

RESULT 10

US-10-059-585-50
; Sequence 50, Application US/10059585
; Publication No. US2003008276A1

GENERAL INFORMATION:

; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE

; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 50

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-059-585-50

Query Match 99.4%; Score 1354; DB 15; Length 403;

Best Local Similarity 99.6%; Pred. No. 1.5e-133;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 63
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 183
Qy 181 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G P T R E D K F N Y P E F 240
Db 184 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G P T R E D K F N Y P E F 243

Qy 241 POPLPVC GD 249
Db 244 POPLPVC GD 252

RESULT 11

US-10-299-003-18
; Sequence 18, Application US/10299003
; Publication No. US20030139324A1

GENERAL INFORMATION:

; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3

; FILE REFERENCE: 2318-385

; CURRENT APPLICATION NUMBER: US/10/299,003

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: U.S. 09/140,749

; PRIOR FILING DATE: 1998-08-26

; PRIOR APPLICATION NUMBER: U.S. 08/791,115

; PRIOR FILING DATE: 1997-01-30

; PRIOR APPLICATION NUMBER: U.S. 60/057,750

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: U.S. 60/083,563

; PRIOR FILING DATE: 1998-04-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 430

; TYPE: PRT

; ORGANISM: Canis familiaris

US-10-299-003-18

Query Match 99.4%; Score 1354; DB 12; Length 430;

Best Local Similarity 99.6%; Pred. No. 1.6e-133;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
Db 40 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 99
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 100 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 159
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 160 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 219
Qy 181 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G P T R E D K F N Y P E F 240
Db 220 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G P T R E D K F N Y P E F 279
Qy 241 POPLPVC GD 249
Db 280 POPLPVC GD 288

RESULT 12

US-10-299-003-15

; Sequence 15, Application US/10299003

; Publication No. US20030139324A1

GENERAL INFORMATION:

; APPLICANT: Steck, Peter

; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jasser, Samar

; APPLICANT: Yung, Alfred W.K.

; APPLICANT: Tavtigian, Sean V.

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3

; FILE REFERENCE: 2318-385

; CURRENT APPLICATION NUMBER: US/10/299,003

```

; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-299-003-15

Query Match
Best Local Similarity 99.4%; Score 1354; DB 12; Length 559;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
D b 160 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 219

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E L I K P F C E D L D O W L S E D D N H V A A I H 120
D b 220 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E L I K P F C E D L D O W L S E D D N H V A A I H 279

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
D b 280 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 339

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y P E F 240
D b 340 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y P E F 399

QY 241 P O P L P V C G D 249
D b 400 P O P L P V C G D 408

```

```

RESULT 13
US-10-299-003-8
; Sequence 8, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Perehouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-299-003-8

Query Match
99.4%; Score 1354; DB 12; Length 597;

```

```

Best Local Similarity 99.6%; Pred. No. 2.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
D b 198 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 257

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E L I K P F C E D L D O W L S E D D N H V A A I H 120
D b 258 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E L I K P F C E D L D O W L S E D D N H V A A I H 317

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
D b 318 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 377

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y P E F 240
D b 378 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y P E F 437

QY 241 P O P L P V C G D 249
D b 438 P O P L P V C G D 446

RESULT 14
US-10-120-801-99
; Sequence 99, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shinketsu, Richard
; APPLICANT: Padigaru, Ramesh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Mehraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott
; APPLICANT: Edinger, Shlomit
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Komuves, Laszlo
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-340
; CURRENT APPLICATION NUMBER: US/10/120,801
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/285748
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/286068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/288334
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/291241
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/322284
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/285609
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 445
; TYPE: PRT
; ORGANISM: human
; US-10-120-801-99

Query Match
37.5%; Score 511; DB 12; Length 445;
Best Local Similarity 44.0%; Pred. No. 5.3e-45;
Matches 103; Conservative 44; Mismatches 75; Indels 12; Gaps 4;

```

```

Query Match      36.3%; Score 494; DB 12; Length 645;
Best Local Similarity 48.8%; Pred. No. 5.3e-43;
Matches 99; Conservative 36; Mismatches 60; Indels 8; Gaps 3;

Qy 1 I I K E I V R N K R R Y Q E G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 60
   : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 319 L T R K L V G N K R R Y K D G F D L D L T V T V T E R I I A M S F P S S G R E S F Y R N P I K V E V R F L D T K P N 378

Qy 61 H Y K I Y N I C A E R H Y T A K P N C R V A Q Y P E D H N P P O L E L I K P C E D L D W L S E D D N H V A A I H 120
   : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 379 H Y O Y N I C S E R A Y Q P K F H Y R V R I M I D D H N V P T L E E M L L P S K V N N M A O D P E N N V A I H 438

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:07 ; Search time 7.19653 Seconds
(without alignments)
3327.436 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 IIKIVSNKRRYQEDGFDL.....RREDKFNFFPQPLPVCGD 249

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514.5	37.8	628	2 T45864	probable tyrosine
2	465	34.1	962	2 T51924	daf-18 protein - C
3	465	34.1	965	2 T32574	hypothetical prote
4	328	24.1	1744	2 A54970	tensin, cardiac mu
5	328	24.1	1792	2 A57075	tensin - chicken (
6	317.5	23.3	1733	2 S27939	tensin - chicken
7	309	22.7	348	2 T40573	protein-tyrosine p
8	286	21.0	1305	2 T31096	cyclin G-associate
9	265	19.5	910	2 S68983	auxilin - bovine
10	244	17.9	434	2 S55155	probable tyrosine
11	187	13.7	264	2 T25762	hypothetical prote
12	144	10.6	537	2 T50099	probable protein-t
13	129	9.5	551	2 S56283	protein-tyrosine-p
14	121.5	8.9	173	2 A56059	protein-tyrosine-p
15	120	8.8	802	1 B44390	protein-tyrosine-p
16	115	8.4	171	1 B47452	dual specificity p
17	111.5	8.2	167	2 J55981	prenylated protein
18	110	8.1	171	1 I36845	dual specificity p
19	110	8.1	171	1 T28522	probable dual spec
20	110	8.1	171	1 B72161	JIL protein - vari
21	110	8.1	1897	1 TDHULK	leukocyte antigen-
22	109	8.0	171	1 QQVZH1	dual specificity p
23	109	8.0	171	1 A42514	dual specificity p
24	108.5	8.0	154	2 I68523	protein tyrosine p
25	108.5	8.0	173	2 J55982	prenylated protein
26	108.5	8.0	190	2 T43172	probable protein-t
27	106	7.8	446	2 T33986	hypothetical prote
28	102	7.5	582	2 A57068	protein-tyrosine-p
29	102	7.5	1290	2 A56493	leucocyte common a

30 100.5 7.4 742 2 F84643
31 100.5 7.4 829 1 A47373
32 100.5 7.4 2302 2 T14328
33 99.5 7.3 394 2 A56115
34 99.5 7.3 796 1 JCL1285
35 99 7.3 668 2 T34317
36 98.5 7.2 218 2 T01111
37 98.5 7.2 802 1 A36085
38 98.5 7.2 1409 2 T42522
39 97 7.1 543 2 AB0850
40 97 7.1 1898 2 S46216
41 96.5 7.1 780 1 JCL1368
42 96 7.0 168 1 A40781
43 94 6.9 1912 2 A56178
44 94 6.9 2029 1 TDFFLK
45 93 6.8 681 2 E88158

ALIGNMENTS

RESULT 1

T45864

Probable tyrosine phosphatase - Arabidopsis thaliana

k;Alternate names: protein F3A4.190

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C;Accession: T45864

R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May

submitted to the Protein Sequence Database, December 1999

A;Reference number: 223007

A;Accession: T45864

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-628 <BAR>

A;Cross-references: EMBL:AL132978

A;Experimental source: cultivar Columbia; BAC clone F3A4

C;Genetics:

A;Map position: 3

A;Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3

A;Note: F3A4.190

Query Match 37.8%; Score 514.5; DB 2; Length 628;

Best Local Similarity 50.0%; Pred. No. 1.1e-38;

Matches 95; Conservative 36; Mismatches 50; Indels 9; Gaps 2;

Qy 3 KEIVSNKRRYQEDGFDLDTIYIPNIAMGFAERL-----EGVYRNIDVVRF 54

Db 181 RHIVSQNRRYQEGFDLDTIYITENIAMGFPAGDISGSLGFFGEGYRNHMEVIRKF 240

Qy 55 DSKHNHYKIYNLCARHYDTAKENCRAVQYFFEDHNPPLQELIKPFCEDLDLSEDDN 114

Db 241 ETHHKDYKYNLCSERLYDASREFGKVASFPFDHNCPPQLIPSCFOSAYTWLKDIQ 300

Qy 115 HVAAIHCKAGKRGVGMICAYLLHGRGFLKAQALDIFYGEVTRDKKGVITPSQRYVY 174

Db 301 NVVVHCKAGMARTGLMCLLLYKFPPTAAEAIYNNQKRCLDGKALVLPSTQIRYVKY 360

Qy 175 YSYLLKNHLD 184

Db 361 YE-RVQNOFD 369

RESULT 2

T51924

daf-18 protein - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C;Accession: T51924

R;Ogg, S.; Ruvkun, G.

Mol. Cell 2, 887-893, 1998

A;Title: The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like metabolic

A;Reference number: 225864

A:Accession: T51924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-962 <OGG>
A:Cross-References: EMBL:AF098286; PIDN:AAD03420.1
C:Genetics:
A:Gene: daf-18

Query Match 34.1%; Score 465; DB 2; Length 962;
Best Local Similarity 41.2%; Pred. No. 5.9e-34;
Matches 93; Conservative 38; Mismatches 85; Indels 10; Gaps 2;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H - K 59
DB 48 I P R T A V S S N R C R T E Y Q N I D D C A Y I T D R I I A I G Y P A T G I E A N F R N S K V Q T Q F L T R H G K 107

QY 60 N H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I 119
DB 108 G N V K V F N L R G G Y Y D A D N F D G N V C F D M T D H H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167

QY 120 H C K A G K R T G V M I C A Y L L H R G F L K A Q E A L D F Y G E V R T D K G V T I P S Q R R V Y Y Y S Y L L 179
DB 168 H C K A G K R T G V M I C A Y L L H R G F L K A Q E A L D F Y G E V R T D K G V T I P S Q R R V Y Y Y S Y L L 179

QY 180 K N H L D Y R P V A L L F H K M W E T I P M F S G G T C N P Q F V V C L K V K I Y S N 225
DB 228 E R E L N Y L P L R M Q L I G V Y R P P T W G G S - - - - - K I R V E V G N 264

RESULT 3
T32574
Hypothetical protein T07A9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32574
R:Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid T07A9.
A:Reference number: Z21194
A:Accession: T32574
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-965 <SCH>
A:Cross-References: EMBL:AF036706; PIDN:AAB92004.1; GSPDB:GN00022; CESP:T07A9.6
A:Experimental source: Strain Bristol N2; clone T07A9
C:Genetics:
A:Gene: CESP:T07A9.6
A:Map position: 4
A:Introns: 71/1; 152/3; 441/2; 642/2; 793/3; 926/3

Query Match 34.1%; Score 465; DB 2; Length 965;
Best Local Similarity 41.2%; Pred. No. 5.9e-34;
Matches 93; Conservative 38; Mismatches 85; Indels 10; Gaps 2;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H - K 59
DB 48 I P R T A V S S N R C R T E Y Q N I D D C A Y I T D R I I A I G Y P A T G I E A N F R N S K V Q T Q F L T R H G K 107

QY 60 N H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I 119
DB 108 G N V K V F N L R G G Y Y D A D N F D G N V C F D M T D H H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167

QY 120 H C K A G K R T G V M I C A Y L L H R G F L K A Q E A L D F Y G E V R T D K G V T I P S Q R R V Y Y Y S Y L L 179
DB 168 H C K A G K R T G V M I C A Y L L H R G F L K A Q E A L D F Y G E V R T D K G V T I P S Q R R V Y Y Y S Y L L 179

QY 180 K N H L D Y R P V A L L F H K M W E T I P M F S G G T C N P Q F V V C L K V K I Y S N 225
DB 228 E R E L N Y L P L R M Q L I G V Y R P P T W G G S - - - - - K I R V E V G N 264

RESULT 4
A54970

tensin, cardiac muscle - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
C:Accession: A54970; S38330; S21544
R:Lo, S.H.; An, Q.; Bao, S.; Wong, W.K.; Liu, Y.; Janney, P.A.; Hartwig, J.H.; Chen, L.B.
J. Biol. Chem. 269, 22310-22319, 1994
A:Title: Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, ex
A:Reference number: A54970; MUID:94350987; PMID:8071358
A:Accession: A54970
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-1744 <LOA>
A:Cross-References: GB:M56625
R:van de Werken, R.; Gemari, M.; Tavella, S.; Bet, P.; Molina, F.; Lin, S.; Cancedda, R.
Eur. J. Biochem. 217, 781-790, 1993
A:Title: Modulation of tensin and vimentin expression in chick embryo developing cartila
A:Reference number: S38330; MUID:94039118; PMID:8223621
A:Accession: S38330
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1469-1744 <VAN>
A:Cross-References: EMBL:X66286; NID:G63802; PIDN:CAA46992.1; PID:G63803
C:Superfamily: SH2 homology
C:Keywords: cardiac muscle; heart
F:1472-1581/Domain: SH2 homology <SH2>

Query Match 24.1%; Score 328; DB 2; Length 1744;
Best Local Similarity 33.8%; Pred. No. 3.3e-21;
Matches 72; Conservative 45; Mismatches 92; Indels 4; Gaps 3;

QY 15 E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K Y K I N L C A E R H Y D 74
DB 62 E S S C E L D L V I T E R I I A V S P T A E Q S F R S N L R E V A H L K S K G D N V L F N L - S E R R H D 120

QY 75 T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H C K A G K R T G V M I C A 134
DB 121 I S K L H P K V L D F G W P D L H T P A L E K I C S I C K A M D T W L N A A A H N V V L H N K N G R L G V V A A 180

QY 135 Y L L H R G F L K A Q E A L D F Y G E V R T D K G V T I - - P S Q R R V Y Y Y S Y L L K N H L D Y R P V A L L F 192
DB 181 Y M H Y S N I S A S A D Q A L D R F A M K R F Y E D K V P V G Q P S Q K R Y I H F S G L L S G S I K M N K P L F L 240

QY 193 H K M W E T I P M F - S G T C N P Q F V V C L K V K I Y S S 224
DB 241 H H V I M H G I P N P E S K G C R P F L K I Y Q A M Q P V I T S 273

RESULT 5
A57075
tensin - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-Jul-2000
C:Accession: A57075
R:Chuang, J.Z.; Lin, D.C.; Lin, S.
J. Cell Biol. 128, 1095-1109, 1995
A:Title: Molecular cloning, expression, and mapping of the high affinity actin-capping d
A:Reference number: A57075; MUID:95204530; PMID:7896874
A:Accession: A57075
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1792 <CHU>
A:Cross-References: GB:L06662; NID:G212754; PIDN:AAA73949.1; PID:G212755
C:Superfamily: SH2 homology
F:1520-1629/Domain: SH2 homology <SH2>

Query Match 24.1%; Score 328; DB 2; Length 1792;
Best Local Similarity 33.8%; Pred. No. 3.4e-21;
Matches 72; Conservative 45; Mismatches 92; Indels 4; Gaps 3;

QY 15 E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K Y K I N L C A E R H Y D 74
DB 110 E S S C E L D L V I T E R I I A V S P T A E Q S F R S N L R E V A H L K S K G D N V L F N L - S E R R H D 168

QY 75 TAKFNCRVAQYPPEDHNPQLEIKPFCELDLWSEDDNVAHAIHCKAGKGRGTGMICA 134
Db ISKLHPKVLDFGWPDLHTPALEKICSIKAMDITWLNAAAHNVVLLHNGRGLGVVAA 228
QY 135 YLLHRGKFLKAQEAALDFYGEVTRDKKGVITI--PSQRRYVYVYLLKNHLDYRVALLF 192
Db 229 YMHYSNISASADQALDRFAMKFEYEDKVPVGPQSQKRYIHYFSGLLSGSIKMNKPLFL 288
QY 193 HKMPEITPMF--SGGTCPNPQFVVCQKVIYSS 224
Db 289 HHVIMHGIPNFESKGCGRPFLLKIYQAMQPVYTS 321
RESULT 6
S27939
tensin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 12-Feb-1999
C:Accession: S27939; S28973
R:Chen, L.B.
submitted to the EMBL Data Library, August 1991
A:Reference number: S27939
A:Accession: S27939
A:Molecule type: mRNA
A:Residues: 1-1733 <CHE>
A:Cross-references: EMBL:M74165; NID:g212751; PID:g212752
R:Weigt, C.; Gaertner, A.; Wegner, A.; Korte, H.; Meyer, H.E.
J. Mol. Biol. 227, 593-595, 1992
A:Title: Occurrence of an actin-inserting domain in tensin.
A:Reference number: S28973; MUID:93021103; PMID:1404377
A:Accession: S28973
A:Molecule type: protein
A:Residues: 862-871, 'X', 873-875, 'A', 877-1212 <WEI>
C:Superfamily: SH2 homology
F:1461-1570/Domain: SH2 homology <SH2>
Query Match 23.3%; Score 317.5; DB 2; Length 1733;
Best Local Similarity 33.6%; Pred. No. 2.9e-20;
Matches 72; Conservative 45; Mismatches 92; Indels 5; Gaps 4;
QY 15 EDGFOLDLTYIYPNIIAMGFAERLE-GVYRNIDVVRFLDSKHKNHYKYNLCARHY 73
Db 62 ESSCEDLVYITERIIVSYPTAEBSFRSLREVAHMLKSKGDNVLFNL-SERRH 120
QY 74 DTAKFNCRVAQYPPEDHNPQLEIKPFCELDLWSEDDNVAHAIHCKAGKGRGTGMIC 133
Db 121 DISKLHPKVLDFGWPDLHTPALEKICSIKAMDITWLNAAAHNVVLLHNGRGLGVVAA 180
QY 134 AYLLHRGKFLKAQEAALDFYGEVTRDKKGVITI--PSQRRYVYVYLLKNHLDYRVALLF 191
Db 181 AMYHYSNISASADQALDRFAMKFEYEDKVPVGPQSQKRYIHYFSGLLSGSIKMNKPLF 240
QY 192 HKMPEITPMF--SGGTCPNPQFVVCQKVIYSS 224
Db 241 LHHVIMHGIPNFESKGCGRPFLLKIYQAMQPVYTS 274
RESULT 7
T40573
protein-tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40573
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21938
A:Accession: T40573
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-348 <SEE>
A:Cross-references: EMBL:AL035226; PIDN:CAA22831.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c609
C:Genetics:

A:Gene: SPAC609.02
A:Map position: 2

Query Match 22.7%; Score 309; DB 2; Length 348;
Best Local Similarity 37.2%; Pred. No. 2.4e-20;
Matches 71; Conservative 37; Mismatches 75; Indels 8; Gaps 4;
QY 1 IIKEIVSRNKRKYQEDGFD-----LDITYIYPNIIAMGFAERLEGVYRNIDVVRFLD 55
Db 3 ILRSVSRGRKGLQKQKVNRSFAYLDVYITSKVIA MSTPAAGIHKLRYNDELDFVKYLT 62
QY 56 SKHKNHYKYNLCARH-YDTAKFNCRVAQYPPEDHNPQLEIKPFCELDLWSEDDN 114
Db 63 TQLKDNWILLNLCAETVYHLELFPKNVINFGODHNPPLFLFLWAIYMNMDALFQTQPL 122
QY 115 HVAAIHCKAGKGRGTGMICAYLLHRGKFLKAQEAALDFYGEVTRDKKGVITPSQRRYVY 174
Db 123 LTLVHVCKAGKGRGTGVICSYLVAFGG-LTAKQSEULEYTEKVMVRGHGLTITSSQIRYVY 181
QY 175 YSYLLKNHLDY 185
Db 182 IE-ILKQFPNY 191

RESULT 8

T31096
cyclin G-associated kinase GAK - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T31096
R:Kanaoka, Y.; Kimura, S.H.; Okazaki, I.; Ikeda, M.; Nojima, H.
FEBS Lett. 402, 73-80, 1997
A:Title: GAK: a cyclin G-associated kinase contains a tensin/auxilin-like domain.
A:Reference number: Z20979; MUID:97165969; PMID:9013862
A:Accession: T31096
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1305 <KAN>
A:Cross-references: EMBL:D38560; NID:g1902912; PIDN:BAA18911.1; PID:g1902913
A:Note: GAK and cyclin G associate together in vivo
C:Genetics:
A:Gene: GAK

Query Match 21.0%; Score 286; DB 2; Length 1305;
Best Local Similarity 32.2%; Pred. No. 1.5e-17;
Matches 67; Conservative 36; Mismatches 87; Indels 18; Gaps 7;

QY 19 LDITYIYPNIIAMGFAERLEGVYRNIDVVRFLDSKHKNHYKYNLCARHYDTAKF 78
Db 405 DLDISYITTSIAVMSFPAEGVESAIKKNIEDVRLFLDAKHPGHVAVYNL-SPRIYRASKF 463
QY 79 NCRVAQYPPEDHNPQLEIKPFCELDLWSEDDNVAHAIHCKAGKGRGTGMICAYLLH 138
Db 464 HNRVTECGWAVRRAPHLHSLYTLCRSMHAWLDHRNVCVVHCDGRAASAVAVCAFLCF 523
QY 139 RGKFLKAQEAALDFYGEVTRDKKGVITPSQRRYVYVYLLKNHLDYRPA-----LLFH 193
Db 524 CRLFSTAEAAVYMFS--MKRCPGGIW-PSHKRYIEYVCDMVAE-----EPIPHSKPMLVK 576
QY 194 KMFETIPMFS--GGTCNPQFVVCQKVIYSS 219
Db 577 SVWMTVPFLFSKQNGCRP---FCEVYV 601

RESULT 9

S68983
auxilin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 08-Oct-1999
C:Accession: S68983
R:Schroeder, S.; Morris, S.A.; Knorr, R.; Plessmann, U.; Weber, K.; Vinh, N.G.; Ungewick
Eur. J. Biochem. 228, 297-304, 1995
A:Title: Primary structure of the neuronal clathrin-associated protein auxilin and its e

A:Reference number: S68983; MUID:95220355; PMID:7705342
A:Accession: S68983
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-910 <SCH>
A:Cross-references: EMBL:U09237; NID:G485268; PIDN:AAA79037.1; PID:G485269
C:Superfamily: dnaJ amino-terminal homology
F:846-910/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 19.5%; Score 265; DB 2; Length 910;
Best Local Similarity 28.8%; Pred. No. 7.7e-16;
Matches 66; Conservative 46; Mismatches 99; Indels 18; Gaps 7;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L - E G V Y R N N I D D V R F L D S K H 60
DB 49 V I Q S T S Y T K G - - - - - D L D T Y T S R I I V M S F P L D S V D I G R N Q V D D I R S F L D S R H L D 101

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q P F E D H N P P Q L E I K P F C E D L D Q L S E D D N H V A A I H 120
DB 102 H T V T N L - S P K S Y R T A K F H S R V S E C S W P I R Q A P S L H N L F A V C R N M Y N W L L Q N P K N V C V H 160

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I - P S O R R Y V Y Y S Y L L 179
DB 161 C L D G R A A S S I L V G A M F I C N L Y S T P G P A V - - - - - R L L Y A K R P G I G L S P S H R R Y L G Y M C D L L 216

QY 180 K N H L D Y R P - V A L L F H K M F E T I P M P S - - G G T C N Q F V V C Q L K V K I Y S S 224
DB 217 A D K - P Y R P H K F L T I K S I T V S P V P F N K O R N C R P Y C D V L I G E T K I Y T T 264

RESULT 10
S55155
probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae)
N:Alternate names: probable tyrosine phosphatase N1220; protein JTB434; protein N1872
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 21-Jul-2000
C:Accession: S55155; S59260; S63073
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
A:Submitted to the EMBL Data Library, November 1994
A:Description: A 43.5 kb fragment of the chromosome XIV.
A:Reference number: S55136
A:Accession: S55155
A:Molecule type: DNA
A:Residues: 1-434 <MAL>
A:Cross-references: EMBL:246843; NID:G861113; PID:G854509
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
Yeast 11, 1195-1209, 1995
A:Title: A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2,
A:Reference number: S59241; MUID:96109932; PMID:8619318
A:Accession: S59260
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-434 <MAL>
A:Cross-references: EMBL:246843; NID:G861113; PID:G854509
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63069
A:Accession: S63073
A:Molecule type: DNA
A:Residues: 1-434 <MAP>
A:Cross-references: EMBL:271404; NID:G1302063; PID:e239804; PID:G1302064; MIPS:YNL128w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:TEP1
A:Cross-references: SGD:S005072; MIPS:YNL128w
A:Map position: 14L
C:Keywords: transmembrane protein
F:38-54/Domain: transmembrane #status predicted <TML>

Query Match 17.9%; Score 244; DB 2; Length 434;
Best Local Similarity 27.6%; Pred. No. 2.5e-14;
Matches 66; Conservative 41; Mismatches 64; Indels 68; Gaps 9;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L - E G V Y R N N I D D V R F L D S K H 58
DB 22 L M K I L S L P M K K T K N D I G L R D I S Y I L V N L I V C S Y P V N T Y P K L L Y R N S L D L I L F L T V Y H 81

QY 59 - K N H Y K I N L C A E R H Y D T A K F N - - - - - C R V A Q P P F E - - - - - 88
DB 82 G K G N F R I P N F R G E K E D S D Y K D N D L I G I T A A K E S K D F E I Q E L R S T L I N D K I P I S P I D L E T 141

QY 89 - - - - - D H N P P Q L E I K P F C E D L D Q L S E D D N H V A A I H C K A G K R T G 129
DB 142 R T L V E E T N N V I C E R I G W L D H F P P P F E L L E I V D G I E N Y L S V S K R V A V L H C R M G K G R S G 201

QY 130 V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R - - - - - T R D K - - - - - K G V T I P S O R R Y V Y Y S Y L L 179
DB 202 M I T W A Y L M - - - - - K Y L Q C P - - - - - L G E A R L I F M Q A R F K Y G M T G N G V T I P S Q L R Y L R V H E F F I 252

RESULT 11
T25762
hypothetical protein F46F11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25762
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid F46F11.
A:Reference number: Z20083
A:Accession: T25762
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-264 <PAU>
A:Cross-references: EMBL:U88173; PIDN:AAB42265.1; GSPDB:GN00019; CESP:F46F11.3
A:Experimental source: strain Bristol N2; clone F46F11
C:Genetics:
A:Gene: CESP:F46F11.3
A:Map position: 1
A:Insertions: 21/3; 43/1; 75/3; 154/2; 182/2; 234/2

Query Match 13.7%; Score 187; DB 2; Length 264;
Best Local Similarity 21.9%; Pred. No. 2e-09;
Matches 56; Conservative 56; Mismatches 120; Indels 24; Gaps 7;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H N 60
DB 15 L V E K L R R K Q R K M D R K E G V Q V E - - Y I T S L I V L S C T S E T S E R K F V E S L L K A S Q Q I Q N A H N K 72

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q P F E D H N P P Q L E I K P F C E D L D Q L S E D D N H V A A I H 120
DB 73 H I R V N V S Q R R H D I S S L D A I P F G W P S E - - T A P S L E K L C T I C K N L D Q M L E H P L N I A V I F 130

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K - - - - - K G V T I P S O R R Y V Y Y S 176
DB 131 C K G G L E R C A I V V N A F M R E N A I S A T D S V D D R F S M Q R P S E R F L G P D G P - - P S Y K R Y L G Y F S 188

QY 177 Y L L K N H L D Y R P V A L L F H K M - - - - - P E T I P M F S G G T C N P Q F V V C Q L K V K I Y S N S G T R R E D 233
DB 189 S L L S G R I S W S D P L Y L H N I L T F F E P I N V F - - - - - L K I Y E R L V P V Y Q S T K V A L N K S S 240

QY 234 K F N V F E P P Q L P V C Q D 249
DB 241 K - - - - F E M D G S L K L R G D 253

RESULT 12
T50099
probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50099
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25037

A;Reference number: S62230
A;Accession: S62239.
A;Molecule type: DNA
A;Residues: 1-551 <MW>
A;Cross-references: EMBL:D44602; NID:g893419; PID:d1008630; PID:g893423
R;Eki, T.; Naitou, M.; Hagiwara, H.; Abe, M.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; T.
Yeast 12, 177-190, 1996
A;Title: Fifteen open reading frames in a 30.8 kb region of the right arm of chromosome
A;Reference number: S63830; MUID:96287654; PMID:8686381
A;Accession: S63833
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-551 <EKI>
A;Cross-references: EMBL:D44602; NID:g893419; PID:d1008630; PID:g893423
R;Shirayama, M.; Matsui, Y.; Toh-e, A.
Mol. Gen. Genet. 251, 176-185, 1996
A;Title: Dominant mutant alleles of yeast protein kinase gene CDC15 suppress the Itel d
A;Reference number: S69234; MUID:96242150; PMID:8668128
A;Accession: S69234
A;Molecule type: DNA
A;Residues: 1-117, 'P', 119-551 <SHI>
A;Cross-references: EMBL:D55715; NID:g870755; PIDN:BAA09533.1; PID:g870756
C;Genetics:
A;Gene: SGD:CDCL4
A;Cross-references: SGD:S0001924; MIPS:YFR028C
A;Map position: 8R
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;283/Active site: Cys (phosphocysteine intermediate) #status predicted
F;289/Binding site: substrate phosphate (Arg) #status predicted

```

Best Local Similarity 26.2%; Pred. NO. 0.00092;
Matches 50; Conservative 27; Mismatches 68; Indels 46; Gaps 9;

Qy 7 SRNRRYQEDGFDLDLTYYIPNIAMGFPAER-----LEGVYRNN 46
Db 166 SYEKYEVEFG---DFNVLTPTDFIASPOEDHPKGYLATKSSHLNQPFKSVLNFANN 222
Qy 47 IDDVVRFDSK--HKNHKYIYNLCARHYDTAKFNCKVAQYPPFDHNPPQLELIKPFCD 104
Db 223 VQLVVR-LNSHLYNKKHFEDIGI---QHLDLI-----FEDGTCPDLSIVKNFVGA 268
Qy 105 LDQWLSEDDNHVAAIHCKAGKGGTGMICAYLLHRGKFLKAQEAALDPYGVRRDKKGV 164
Db 269 AETIIKRGK--IAVHCKAGLRTGCLIGAHLIYTYGF-TANECIGFLRFIR----PGM 321
Qy 165 IPSORRYVYYY 175
Db 322 VGPQHWLYLH 332

RESULT 14
A56059
protein-tyrosine-phosphatase (EC 3.1.3.48) PRL-1 - rat
C:Species: Rattus sp. (rat)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 08-Oct-1999
C:Accession: A56059
R:Diamond, R.H.; Cressman, D.E.; Laz, T.M.; Abrams, C.S.; Taub, R.
Mol. Cell. Biol. 14, 3752-3762, 1994
A:Title: PRL-1, a unique nuclear protein tyrosine phosphatase, affects cell growth.
A:Reference number: A56059; MUID:94254833; PMID:8196618
A:Accession: A56059
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-173 <DIA>
A:Cross-references: GB:I27843; NID:G530161; PIDN:AAA41935.1; PID:G530162
C:Keywords: immediate-early protein; nucleus; phosphoric monoester hydrolase; tyrosine-s

Query Match 8.9%; Score 121.5; DB 2; Length 173;
Best Local Similarity 27.5%; Pred. No. 0.0011;
Matches 50; Conservative 23; Mismatches 52; Indels 57; Gaps 11;

Qy 32 MGPAERLEGVYRNNIDVVRFI-----DSKHNHYKIYNLCARHYDTA 76

```

Job time : 9.19653 secs

```
Db      4  MRPPAP-VEVYTKN-----MRLLTHNPTNATLNKFEIELKKYGVTTIVRVC-EATYDTT 56
QY      77  ---KFCNRVAQYFFEDHNPQLELKPFCEDLDQMLS-----EDDNHVAAIHCKAGKG 126
Db      57  LVEKEGIHVLDPFDGAPPSNQIV-----DWLSLVKIKFREEPGCCIAVHCVAGLG 109
QY      127 RTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTFPSORRYVYYSYLLKNHLD-Y 185
Db      110 RAPVLVALALIEGG--MKYEDAVQF-----IRQKRGAFNSKOLL--YLEKY 152
QY      186 RP 187
Db      153 RP 154

RESULT 15
B44390.
protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse
N:Alternate names: protein-tyrosine-phosphatase PEP
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence revision 26-May-1994 #text_change 11-Jun-1999
C:Accession: B44390; S71952; S27876
R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases:
, and threonine-rich sequences.
A:Reference number: A44390; MUID:92236615; PMID:1373816
A:Accession: B44390
A:Molecule type: mRNA
A:Residues: 1-802 <MAT>
A:Cross-references: GB:M90388; NID:G200522; PIDN:AAA39994.1; PID:G200523
R:Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4909-4918, 1996
A:Title: Association of inhibitory tyrosine protein kinase p50 (csk) with protein tyrosin
A:Reference number: S71952; MUID:97045099; PMID:8890164
A:Accession: S71952
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 495-789 <CLO>
C:Comment: This protein is found primarily in hematopoietic tissues.
C:Genetics:
A:Gene: 70zpep
C:Complex: physically associates with inhibitory tyrosine protein kinase Csk; interactio
C:Function:
A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosph
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:54-278/Domain: protein-tyrosine-phosphatase homology <PTP>
F:497-802/Region: glutamic acid/proline/serine/threonine-rich
F:613-621/Region: proline-rich
F:688-695/Region: proline-rich
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match      8.8%; Score 120; DB 1; Length 802;
Best Local Similarity 32.5%; Pred. No. 0.0095;
Matches 49; Conservative 16; Mismatches 44; Indels 42; Gaps 10;

QY      57  KHKNHKYNLCAERHYDTAKENCR---VAQYPPF---DHNPPQ-----LELIKPFCEDL 105
Db      164  KKKSDYKIRTL-----KAKFNNETRIYQHYKNWPDHVPSSIDPILQLI----- 209
QY      106  DQW-----LSEDDNHVAIHCAGKRGTMICA-----YLLHRGKFLKAQALDFYGEVR 156
Db      210  --WDMRCYQEDDCVPICIHCSAGCGRTGV-ICAVDYTWMLLKDGIIIPKNFSVFNLIQEMR 266
QY      157  TRDKKGVTFPSORRYVYYSYLL---KNHLD 184
Db      267  T--QRPSLVQTEQVELVYSVAVLELFXRHMD 295
```

Search completed: December 10, 2003, 20:34:59

GenCore version 5.1.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:57 ; Search time 4.31792 Seconds
(without alignments)
2711.873 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 LIKEIVSNKRYQEDGFDL.....RREDKFNYPFPQPLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1354	99.4	403	PTEN_HUMAN	O00633 homo sapien
2	1354	99.4	403	PTEN_MOUSE	O08586 mus musculu
3	478	35.1	551	TPTE_HUMAN	P56180 homo sapien
4	328	24.1	1744	TENS_CHICK	O04205 gallus gall
5	286	21.0	1305	GAK_RAT	P97874 rattus norv
6	285	20.9	1311	GAK_HUMAN	O14976 homo sapien
7	265	19.5	910	AUX1_BOVIN	Q27974 bos taurus
8	244	17.9	434	YNM8_YEAST	P53916 saccharomyc
9	187	13.7	264	YLPK_CAEEL	P91301 caenorhabdi
10	144	10.6	537	FLP1_SCHPO	Q09771 schizosacch
11	129	9.5	551	CL14_YEAST	Q00684 saccharomyc
12	120	8.8	802	PTN8_MOUSE	P29352 mus musculu
13	115	8.4	171	VH01_RACVI	P80994 racoon pox
14	110	8.1	171	DUSP_VARV	P33064 variola vir
15	110	8.1	1897	PTPF_HUMAN	P10586 homo sapien
16	109	8.0	171	DUSP_VACCC	P20495 vaccinia vi
17	109	8.0	171	DUSP_VACCV	P07239 vaccinia vi
18	102.5	7.5	807	PTNM_HUMAN	O9v2r2 homo sapien
19	100.5	7.4	829	PTRA_MOUSE	P18052 mus musculu
20	99.5	7.3	796	PTRA_RAT	Q03348 rattus norv
21	98.5	7.2	802	PTRA_HUMAN	P18433 homo sapien
22	96.5	7.1	168	PTP_NPVAC	Q05209 homo sapien
23	96	7.0	178	PTNC_HUMAN	P24656 autographa
24	95.5	7.0	178	DUSP_MXVVL	Q85297 myxoma viru
25	94	6.9	1312	PTPD_HUMAN	P23468 homo sapien
26	94	6.9	2029	LAR_DROME	P16621 drosophila
27	93	6.8	1063	CDCE_CAEEL	P81299 caenorhabdi
28	92.5	6.8	394	DUSA_HUMAN	Q13115 homo sapien
29	92.5	6.8	395	DUSA_RAT	Q62767 rattus norv
30	92.5	6.8	775	PTNC_MOUSE	P35831 mus musculu
31	92	6.8	2200	LAR_CAEEL	Q9bm8 caenorhabdi
32	91.5	6.7	1301	PTP9_DROME	P35832 drosophila
33	90.5	6.6	482	DUSA_HUMAN	Q9y6w6 homo sapien

ALIGNMENTS

RESULT 1

```
PTEN_HUMAN
ID PTEN_HUMAN STANDARD; PRT; 403 AA.
AC O00633; O02679;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1 OR TEP1.
OS Homo sapiens (Human), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9615;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC SPECIES=Human, and C.familiaris;
RX MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Pershouse W.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattier T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.;
RA "Identification of a candidate tumour suppressor gene, MMAC1, at
RT chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=97228181; PubMed=9072974;
RA Li J., Yen C., Liaw D., Podsypanina K., Bose S., Wang S.L., Puc J.,
RA Miliaretsis C., Rodgers L., McCombie R., Bigner S.H., Giovanella B.C.,
RA Ittmann M., Tycko B., Hibshoosh H., Wigler M.H., Parsons R.;
RT "PTEN, a putative protein tyrosine phosphatase gene mutated in human
RL brain, breast, and prostate cancer.";
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=97330649; PubMed=9187108;
RA Li D.M., Sun H.;
RT "TP1, encoded by a candidate tumor suppressor locus, is a novel
RL protein tyrosine phosphatase regulated by transforming growth factor
beta.";
RN [4]
RP Cancer Res. 57:2124-2129(1997).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=97330649; PubMed=9187108;
RA Wang S., Li J., Liaw D., Bose S., Podsypanina K., Parsons R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=97330649; PubMed=9187108;
RA Jensen K., de la Bastide M., Parsons R., Parnell L.D., Dedhia N.,
RA Gottesman T., Gnoj L., Kaplan N., Lochi M., Johnson A.F., Shohdy N.,
RA Hasegawa A., Haberman K., Huang E.N., Schutz K., Calma C., Granat S.,
RA Wigler M., McCombie W.R.;
```

RT "Genomic sequence of PTEN/MMAC1.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [16]
RC SEQUENCE FROM N.A.
RA SPECIES=Human;
RC Gray N.E., Stewart L.M.D., Hamilton J.A., Roberts K.G., Watson G.,
RA Snary D.;
RT "Genomic sequence of chromosome 10q23.3 containing exons 6, 7, 8 and 9
of the PTEN gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [17]
RC SEQUENCE FROM N.A.
RA SPECIES=Human;
RC Tissue=Lung;
RX MEDLINE=22368357; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Itohlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [18]
RC CHARACTERIZATION.
RP VARIANT B2S ARG-170.
RC SPECIES=Human;
RX MEDLINE=97404346; PubMed=9256433;
RA Myers M.P., Stolarov J.P., Eng C., Li J., Wang S.I., Wigler M.H.,
RA Parsons R., Tonks N.K.;
RT "p-TEN, the tumor suppressor from human chromosome 10q23, is a dual-
specificity phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9052-9057(1997).
RN [19]
RC FUNCTION.
RC SPECIES=Human;
RX MEDLINE=98256248; PubMed=9593664;
RA Maehama T., Dixon J.E.;
RT "The tumor suppressor, PTEN/MMAC1, dephosphorylates the lipid second
messenger, phosphatidylinositol 3,4,5-trisphosphate.";
RL J. Biol. Chem. 273:13375-13378(1998).
RN [10]
RP PHOSPHORYLATION OF THR-366; SER-370 AND SER-385.
RC SPECIES=Human;
RX MEDLINE=22237351; PubMed=12297295;
RA Miller S., Low D., Seldin D., Lane W., Neel B.;
RT "Direct identification of PTEN phosphorylation sites.";
RL FEBS Lett. 528:145-145(2002).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.10 ANGSTROMS) OF 7-353.
RC SPECIES=Human;
RX MEDLINE=20021619; PubMed=10555148;
RA Lee J.-O., Yang H., Georgescu M.-M., Di Cristofano A., Maehama T.,
RA Shi Y., Dixon J.E., Pandolfi P., Pavlath N.P.;
RT "Crystal structure of the PTEN tumor suppressor: implications for its
phosphoinositide phosphatase activity and membrane association.";
RL Cell 99:323-334(1999).
RN [12]
RP VARIANT CD ASN-137 INS.
RC SPECIES=Human;
RX MEDLINE=98007985; PubMed=9345101;
RA Tsou H.C., Teng D.H.-F., Ping X.L., Brancolini V., Davis T., Hu R.,
RA Xie X.X., Gruener A.C., Schrager C.A., Christiano A.M., Eng C.,
RA Steck P., Ott J., Tavtigian S.V., Peacocke M.;
RT "The role of MMAC1 mutations in early-onset breast cancer: causative
in association with Cowden syndrome and excluded in BRCA1-negative
cases.";
RL Am. J. Hum. Genet. 61:1036-1043(1997).
RN [13]
RP VARIANTS CD GLU-343 AND LEU-347.
RC SPECIES=Human;
RX MEDLINE=98153621; PubMed=9399897;
RA Lynch E.D., Ostermeyer E.A., Lee M.K., Arena J.F., Ji H., Dann J.,
RA Swisshelm K., Suchard D., Macleod P.M., Kvinnelsland S., Gjertsen B.T.,
RA Heimdal K., Lubs H., Moeller P., King M.-C.;
RT "Inherited mutations in PTEN that are associated with breast cancer,
Cowden disease, and juvenile polyposis.";
RL Am. J. Hum. Genet. 61:1254-1260(1997).
RN [14]
RP VARIANTS CD ARG-123 AND ARG-124.
RC SPECIES=Human;
RX MEDLINE=97402224; PubMed=9259288;
RA Neelen M.R., van Staveren W.C.G., Peeters E.A.J., Ben Hassel M.,
RA Gorlin R.J., Hamm H., Lindboe C.F., Fryns J.-P., Sijmons R.H.,
RA Woods D.G., Mariman E.C.M., Padberg G.W., Kremer H.;
RT "Germline mutations in the PTEN/MMAC1 gene in patients with Cowden
disease.";
RL Hum. Mol. Genet. 6:1383-1387(1997).
RN [15]
RP VARIANT CD GLU-129.
RC SPECIES=Human;
RX MEDLINE=97285123; PubMed=9140396;
RA Liaw D., Marsh D.J., Li J., Dahia P.L.M., Wang S.I., Zheng Z.,
RA Rose S., Call K.M., Tsou H.C., Peacocke M., Eng C., Parsons R.;
RT "Germline mutations of the PTEN gene in Cowden disease, an inherited
breast and thyroid cancer syndrome.";
RL Nat. Genet. 16:64-67(1997).
RN [16]
RP VARIANT B2S ARG-170.
RC SPECIES=Human;
RX MEDLINE=9738233; PubMed=9241266;
RA Marsh D.J., Dahia P.L.M., Zheng Z., Liaw D., Parsons R., Gorlin R.J.,
RA Eng C.;
RT "Germline mutations in PTEN are present in Bannayan-Zonana syndrome.";
RL Nat. Genet. 16:333-334(1997).
RN [17]
RP VARIANT CD GLU-289.
RC SPECIES=Human;
RX MEDLINE=99014194; PubMed=9797362;
RA Chi S.-G., Kim H.-J., Park B.-J., Min H.-J., Park J.-H., Kim Y.-W.,
RA Dong S.-H., Kim B.-H., Lee J.-I., Chang Y.-W., Chang R., Kim W.-K.,
RA Yang M.-H.;
RT "Mutational abrogation of the PTEN/MMAC1 gene in gastrointestinal
polyps in patients with Cowden disease.";
RL Gastroenterology 115:1084-1089(1998).
RN [18]
RP VARIANTS CD HIS-68 AND PRO-112.
RC SPECIES=Human;
RX MEDLINE=98260873; PubMed=9600246;
RA Tsou H.C., Ping X.L., Xie X.X., Gruener A.C., Zhang H., Nini R.,
RA Swisshelm K., Sybert V., Diamond T.M., Sutphen R., Peacocke M.;
RT "The genetic basis of Cowden's syndrome: three novel mutations in
PTEN/MMAC1/TP1.";
RL Hum. Genet. 102:467-473(1998).
RN [19]
RP VARIANTS CD AND B2S.
RC SPECIES=Human;
RX MEDLINE=98133933; PubMed=9467011;
RA Marsh D.J., Coulon V., Lunetta K.L., Rocca-Serra P., Dahia P.L.M.,
RA Zheng Z., Liaw D., Caron S., Duboue B., Lin A.Y., Richardson A.-L.,
RA Bonnetblanc J.-M., Bressieux J.-M., Cabaret-Moreau A., Chompert A.,
RA Demange L., Reles R.A., Yahanda A.M., Fearon E.R., Fricker J.-P.,
RA Gorlin R.J., Hodgson S.V., Huson S., Lacombe D., Leprat F., Odent S.,
RA Toulouse C., Olopade O.I., Sobol H., Tishler S., Woods C.G.,
RA Robinson B.G., Weber H.C., Parsons R., Peacocke M., Longy M., Eng C.;

Query Match 99.4%; Score 1354; DB 1; Length 403;
Best Local Similarity 99.6%; Pred. No. 6.9e-121;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G T R R E D K E N Y F E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G T R R E D K E N Y F E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 2

ID PTEN MOUSE
AC O08586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Pershouse M.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattvig T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.;
RT "Identification of a candidate tumour suppressor gene, MMAC1, at
RT chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
CC -!- FUNCTION: Potential tumor suppressor. Acts as a phosphoinositide
CC 3-phosphatase by regulating PtdIns(3,4,5)P3 levels.
CC -!- CATALYTIC ACTIVITY: Phosphatidylinositol-3,4,5-trisphosphate +
CC H(2)O = phosphatidyl inositol-4,5-bisphosphate + phosphate.
CC -!- COFACTOR: Magnesium.
CC -!- PTM: Phosphorylation results in an inhibited activity towards
CC PIP3 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC DB EMBL; U92437; AAC53118.1; -.
DB MGD; MGI:109583; Pten.
DR GO; GO:0016506; F:apoptosis activator activity; IMP.
DR GO; GO:0016314; F:phosphatidylinositol-3,4,5-trisphosphate 3-...; IDA.
DR GO; GO:0016477; P:cell migration; IMP.

DR GO; GO:0007417; P:central nervous system development; IMP.
DR GO; GO:0006917; P:induction of apoptosis; IMP.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
KW Hydrolase; Anti-oncogene; Phosphorylation.
FT DOMAIN 22 303
FT ACT_SITE 124 124
FT MOD_RES 366 366
FT MOD_RES 370 370
FT MOD_RES 385 385
SQ SEQUENCE 403 AA; 47152 MW; 75F97C3DD6843BA9 CRC64;

Query Match 99.4%; Score 1354; DB 1; Length 403;
Best Local Similarity 99.6%; Pred. No. 6.9e-121;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G T R R E D K E N Y F E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G T R R E D K E N Y F E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 3
ID PTEN HUMAN
AC P56180;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative protein-tyrosine phosphatase TPTE (EC 3.1.3.48).
GN TPTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=restis;
RX MEDLINE=20063863; PubMed=10598804;
RA Chen H., Rossier C., Morris M.A., Scott H.S., Gos A., Bairoch A.,
RA Antonarakis S.E.;
RT "A testis-specific gene, TPTE, encodes a putative transmembrane
RT tyrosine phosphatase and maps to the pericentromeric region of human
RT chromosomes 21 and 13, and to chromosomes 15, 22, and Y.";
RL Hum. Genet. 105:399-409(1999).
CC [2]
CC SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Negamine K., Mitsuoyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek K., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,

RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Niretic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21";
RL Nature 405:311-319(2000).
CC -!- FUNCTION: COULD BE INVOLVED IN SIGNAL TRANSDUCTION.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN TESTIS.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007118; AAC34574.1; -;
DR EMBL; AL163201; CAB90528.1; -;
DR Genew; HGNC:12023; TTE.
DR MIM; 604336; -;
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR005820; M+channel nlg.
DR InterPro; IPR000387; TYR phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR Hydrolase; Transmembrane.
KW TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 164 194 POTENTIAL.
FT DOMAIN 236 518 TENSIN.
FT ACT_SITE 338 338 POTENTIAL.
FT CONFLICT 386 386 E -> K (IN REF. 2).
FT CONFLICT 470 470 P -> L (IN REF. 2).
SQ SEQUENCE 551 AA; 64307 MW; 39C031C7D30685D2 CRC64;

Query Match 35.1%; Score 478; DB 1; Length 551;
Best Local Similarity 38.4%; Pred. No. 1.2e-37;
Matches 103; Conservative 48; Mismatches 83; Indels 34; Gaps 5;

QY 1 I I K E I V S R K R Y O E D G F D L D T Y I P N I A M G F P A E R L E G V Y R N N I D D V R F L D S K H Q N 60
DB 218 L I R R V S E N K R Y R D G F D L D T Y T E R I A M S F S S G R Q S Y R N P I K E V R F L D K H R N 277

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H P N P Q L E I K P F C E D L D W L S E D D N H V A I H 120
DB 278 H Y R V N L C S E R A Y D P R K F H N R V R I M D D H N V P T L H Q M V V F T K E V N E W A Q L E N I V A I H 337

QY 121 C K A G K R T G M V C A Y L L H R G K E L K A Q E A L D F G E V R T R K - - - - - K G V T I S Q R Y V Y 174
DB 338 C K G G T D R T G M V C A F L I A S E I C S T A K E S L Y F G E R T - D K T H S K P Q G V E T S Q R Y V A Y 396

QY 175 Y S - - - Y L L K N H L D Y R V A L L F H - - - - - K W F E T I P M F S G T C N P 210
DB 397 P A Q V K H L Y N W N L P P R I L I K F I I Y S I P R Y R D L K I Q I E M E K K V F S T I S L - - - G K C S V 453

QY 211 Q F V V C L K V K I Y S N S G P T R R E D K F N Y F 238
DB 454 L D N I T T D K I L D V F D G P L Y D V K V Q F F 481

RESULT 4
TENS_CHK
ID TENS_CHK
AC Q04205; Q91007; Q92011;
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Tensin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=94350987; PubMed=8071358;
RA Lo S.H., An Q., Bao S., Wong W.K., Liu Y., Janney P.A., Hartwig J.H.,
RA Chen L.B.;
RT "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA
RT sequence, expression, and characterization.";
RL J. Biol. Chem. 269:22310-22319(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95204530; PubMed=7896874;
RA Chuang J.Z., Lin D.C., Lin S.;
RT "Molecular cloning, expression, and mapping of the high affinity
RT actin-capping domain of chicken cardiac tensin.";
RL J. Cell Biol. 128:1095-1109(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC Chen L.B.;
RA Submitted (XXX-1991) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE OF 1469-1744 FROM N.A.
RC TISSUE=Embryonic chondrocytes, and Embryonic heart;
RX MEDLINE=94039118; PubMed=8223621;
RA van de Werken R., Gennari M., Tavella S., Bet P., Molina F.,
RA Lin S., Cancedda R., Castagnola P.;
RT "Modulation of tensin and vimentin expression in chick embryo
RT developing cartilage and cultured differentiating chondrocytes.";
RL Eur. J. Biochem. 217:781-790(1993).
RN [5]
RP SH2 DOMAIN.
RX MEDLINE=91220073; PubMed=1708917;
RA Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,
RA Roberts T.M., An Q., Chen L.B.;
RT "Presence of an SH2 domain in the actin-binding protein tensin.";
RL Science 252:712-715(1991).
CC -!- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT
CC AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.
CC BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED
CC CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.
CC -!- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.
CC -!- TISSUE SPECIFICITY: HEART, GIZZARD, LUNG AND SKELETAL MUSCLE.
CC -!- PTM: TYROSINE-PHOSPHORYLATED.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96625; AAA59053.1; -;
DR EMBL; L06662; AAA73949.1; ALT_INIT.
DR EMBL; Z18529; CAA79215.1; ALT_INIT.
DR EMBL; M74165; AAA49087.1; -;
DR EMBL; X66286; CAA46992.1; -;
DR PIR; A54970; A54970.
DR PIR; S27939; S27939.
DR HSSP; P16277; 1BLK.
DR InterPro; IPR006020; PTB_P1D.
DR InterPro; IPR000980; SH2-

```
DR Pfam: PF00017; SH2; 1.  
DR ProDom: PD000093; SH2; 1.  
DR SMART: SM00462; PRT; 1.  
DR SMART: SM00252; SH2; 1.  
DR PROSITE: PS00001; SH2; 1.  
KW Actin-binding; Cytoskeleton; SH2 domain; Phosphorylation.  
FT DOMAIN 66 342  
FT DOMAIN 1472 1581  
FT CONFLICT 49 49  
FT CONFLICT 61 61  
FT CONFLICT 88 88  
FT CONFLICT 404 404  
FT CONFLICT 452 452  
FT CONFLICT 508 508  
FT CONFLICT 522 522  
FT CONFLICT 664 664  
FT CONFLICT 666 666  
FT CONFLICT 875 875  
FT CONFLICT 909 909  
FT CONFLICT 1102 1102  
FT CONFLICT 1240 1240  
FT CONFLICT 1480 1480  
FT CONFLICT 1711 1711  
SQ SEQUENCE 1744 AA; 187214 MW; 5C3CB6211935524 CRC64;  
  
Query Match 24.1%; Score 328; DB 1; Length 1744;  
Best Local Similarity 33.8%; Pred. No. 8.4e-23;  
Matches 72; Conservative 45; Mismatches 92; Indels 4; Gaps 3;  
  
QY 15 EDGFDLDLYIPNIIANGFAERLEGVYRNIDVDFLDSKHKNHYKYNLCARHYD 74  
DB 62 EESCELDLYITRIIAVSPYTABEQSFRSLREVAHMLKSKGNDGYVLFNL-SERRHD 120  
QY 75 TAKFRCRVAQYPFEDHNPQLEIKPFCEDLDLSEDDNHVAAIHCAGKGRGTGMICA 134  
DB 121 ISKLHPKVLDFGPDILHTPALEKICSIKAMDTLNAAHNVVVLHNGRGLGVVAA 180  
QY 135 YLLHKGKFLKAQALDFYGEVTRDKKGVTI--PSQRYVYVYVYVYVYVYVYVYV 192  
DB 181 YMHYSNISASDAQDQALDFAMKRFYEDKVPVQSPQSKRYHYFVSGLLSGSKMKNKPLFL 240  
QY 193 HKMPEITPMF--SGTCNPQFVVCOLVKIYSS 224  
DB 241 HHVIMHGIPNFSKGGCRPFLKIYQAMQPVYTS 273  
  
RESULT 5  
GAK_RAT  
ID GAK_RAT STANDARD; PRT; 1305 AA.  
AC P97874;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cyclin G-associated kinase (EC 2.7.1.-).  
GN GAK.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97165969; PubMed=9013862;  
RA Kanaka Y., Kimura S.H., Okazaki I., Ikeda M., Nojima H.;  
RT "GAK: a cyclin G associated kinase contains a tensin/auxilin-like domain.";  
RL FEBS Lett. 402:73-80(1997).  
CC -!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an  
CC auxilin homolog that is involved in the uncoating of clathrin-  
CC coated vesicles by Hsc70 in non-neuronal cells. Expression  
CC oscillates slightly during the cell cycle, peaking at G1 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the  
  
trans-Golgi network. Also seen on the plasma membrane, probably at  
focal adhesions (By similarity).  
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
-!- SIMILARITY: Contains 1 tensin domain.  
-!- SIMILARITY: Contains 1 J domain.  
-!- SIMILARITY: Contains 1 J domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: D38560; BRA18911.1; -  
DR PIR: T31096; T31096.  
DR InterPro: IPR001623; DnaJ_N.  
DR InterPro: IPR000719; Prot_kinase.  
DR InterPro: IPR002290; Ser_thr_kinase.  
DR Pfam: PF00226; DnaJ; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Prot_kinase; 1.  
DR SMART: SM00271; DnaJ; 1.  
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.  
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.  
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.  
DR PROSITE: PS00636; DnaJ_1; FALSE_NEG.  
DR PROSITE: PS00076; DnaJ_2; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Nuclear protein; Endoplasmic reticulum; Cell cycle.  
FT DOMAIN 40 315  
FT ACT SITE 173 173  
FT DOMAIN 405 689  
FT DOMAIN 1241 1305  
FT J-DOMAIN  
SQ SEQUENCE 1305 AA; 143702 MW; 6D36BD38011C44EE CRC64;  
  
Query Match 21.0%; Score 286; DB 1; Length 1305;  
Best Local Similarity 32.2%; Pred. No. 5.6e-19;  
Matches 67; Conservative 36; Mismatches 87; Indels 18; Gaps 7;  
  
QY 19 DLDLYIPNIIANGFAERLEGVYRNIDVDFLDSKHKNHYKYNLCARHYDTAKF 78  
DB 405 DLDISYITSTIAVMSFPAEGVESAIKNIEDVRLFLDAKHGPHYAVNLT-SPRIYRASKF 463  
QY 79 NCRVAQYPFEDHNPQLEIKPFCEDLDLSEDDNHVAAIHCAGKGRGTGMICAYLLH 138  
DB 464 HNRVTECGWAVRRAPHLHSLYTLCSHMAWLRDHRNVVVCVHCDGRAASAVAVCAFLCF 523  
QY 139 RGKFLKAQALDFYGEVTRDKKGVTI--PSQRYVYVYVYVYVYVYVYVYV 193  
DB 524 CRLFTAEAAVYMF--MKRCPGGI--PSHKRYIEYVCDMVAE---EPITPHSKPMLVK 576  
QY 194 KMWETIPMFS--GGTCNPQFVVCOLKV 219  
DB 577 SVVMTVPVLFSGKQRCRP---FCEVYV 601  
  
RESULT 6  
GAK_HUMAN  
ID GAK_HUMAN STANDARD; PRT; 1311 AA.  
AC O14976; Q9BVY6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Cyclin G-associated kinase (EC 2.7.1.-).  
GN GAK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Fibroblast;
```

MEDLINE=9746136; PubMed=9299234;
Kimura S.H., Tsuruga H., Yabuta N., Endo Y., Nojima H.;
"Structure, expression, and chromosomal localization of human GAK.";
Genomics 44:179-187(1997).
[2]
SEQUENCE OF 981-1311 FROM N.A.
TISSUE=Placenta;
MEDLINE=23389257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshikiyuki S., Carncini P., Prange C.,
Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
FUNCTION, AND SUBCELLULAR LOCATION.
MEDLINE=20092914; PubMed=10625686;
Greener T., Zhao X., Nojima H., Eisenberg E., Greene L.E.;
"Role of cyclin G-associated kinase in uncoating clathrin-coated
vesicles from non-neuronal cells";
J. Biol. Chem. 275:1365-1370(2000).
-!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an
auxilin homolog that is involved in the uncoating of clathrin-
coated vesicles by Hsc70 in non-neuronal cells. Expression
oscillates slightly during the cell cycle, peaking at G1.
-!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the
trans-Golgi network. Also seen on the plasma membrane, probably at
focal adhesions.
-!- TISSUE SPECIFICITY: Ubiquitous. Highest in testis.
-!- SIMILARITY: BELONGS TO THE SPR/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: Contains 1 tensin domain.
-!- SIMILARITY: Contains 1 J domain.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; D88435; BAA22623.1; --
EMBL; BC008815; AAH00815.1; --
EMBL; CC008658; AAH08658.1; --
GeneID; HGNC:4113; GAK.
MIM; 602052; --
GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00226; DnaJ_1.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00271; DnaJ_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00111; PROTEIN_KINASE_DTP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00636; DNAJ_1; FALSE_NEG.

DR PROSITE; PS50076; DNAI_2; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KL Nuclear protein; Endoplasmic reticulum; Cell cycle.
 FT DOMAIN 40 314 PROTEIN KINASE.
 FT ACT SITE 173 173 BY SIMILARITY.
 FT DOMAIN 347 350 POLY-PRO.
 FT DOMAIN 407 691 TENSIN.
 FT DOMAIN 1247 1311 J-DOMAIN.
 FT CONFLICT 1113 1113 P -> A (IN REF. 1).
 SQ SEQUENCE 1311 AA; 143190 MW; OACE45DF57A5F981 CRC64;

Query Match 20.98; Score 285; DB 1; Length 1311;
 Best Local Similarity 29.48; Pred. No. 7e-19;
 Matches 73; Conservative 47; Mismatches 96; Indels 32; Gaps 10

QY 19 DLDLTITYPNIAMGPPAEERLEGVYRNIDVVRFLDSKHKHVKIYNLCARHYDITAKF 78
 DB 407 DLDISVITSIAVMSPPAEGVESALKNNIEDVRLFLDSKHPGHAVYNL-SPRTYRPSRF 465
 QY 79 NCRVAQYPPFDHNPPLQLELIPFCEDDQWLSEDDNHVAAIHCXAGKGRGTGMICAYLLH 138
 DB 466 HNRVSECGAARRAPHLHTLYNICRNHMWLRQDHKNVCVHCHMDGRAASAVAVCSFLCF 525
 QY 139 RGFLKRAQELDPYGEVRTDKGVITPSSRRYVYVSYLLKQHLDRPVA-----LLFH 193
 DB 526 CRLFEATAEAAYVMS--MKRCPGIIW-PSHKRIEYNCMDVMAE---EPITPHSKPILVR 578
 QY 194 KMFETIPMS--GGTCNPQFVVCOLKV--KIYSSNGPTRRREDKFNYPF-----FP 241
 DB 579 AVVTPVPLFSKQSGCRP---FCEVIVGDERVAST-----SQEYDKMRDFKIEDGKAVIP 631
 QY 242 QPLPVCGD 249
 DB 632 LGVTVQGD 639

RESULT 7
 AUX1_BOVIN STANDARD; PRT; 910 AA.
 ID AUX1_BOVIN STANDARD; PRT; 910 AA.
 AC Q2797a;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Auxilin.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95220355; PubMed=7705342;
 RA Schroeder S., Morris S.A., Knorr R., Plesmann U., Weber K.,
 RT Vinh N.G., Ungewickell E.;
 RT "Primary structure of the neuronal clathrin-associated protein
 RT auxilin and its expression in bacteria.";
 RL Eur. J. Biochem. 228:297-304(1995).
 RC -1- FUNCTION: BINDS CLATHRIN HEAVY CHAIN AND PROMOTES ITS ASSEMBLY
 CC INTO REGULAR CAGES.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- PTM: TARGET FOR COAT-ASSOCIATED CASEIN KINASE II IN VITRO.
 CC -1- SIMILARITY: Contains 1 tensin domain.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/ebis/sib.ch>).
 CC or send an email to license@ebi.ac.uk.

```
-----
CC EMBL; U09237; AAA79037.1; -.
CC PIR; S68983; S68983.
CC InterPro; IPR001623; DnaJ_N.
CC Pfam; PF00226; DnaJ_1.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; UNKNOWN_1.
CC PROSITE; PS00636; DnaJ_1; FALSE_NEG.
CC PROSITE; PS00076; DnaJ_2; 1.
KW SH3-binding; Repeat; Phosphorylation.
FT DOMAIN 33 44
FT REPEAT 33 36
FT REPEAT 37 40
FT REPEAT 41 44
FT DOMAIN 60 344
FT SITE 406 414 SH3-BINDING (POTENTIAL).
FT DOMAIN 463 757 PRO-RICH.
FT DOMAIN 526 529 POLY-GLY.
FT DOMAIN 846 910 J-DOMAIN.
SQ SEQUENCE 910 AA; 99512 MW; BC156DC1CF3487FD CRC64;

Query Match 19.5%; Score 265; DB 1; Length 910;
Best Local Similarity 28.8%; Pred. No. 3.5e-17;
Matches 66; Conservative 46; Mismatches 99; Indels 18; Gaps 7;

QY 1 I I K E I V S R K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G Y V R N N I D D V V R F L D S K H N 60
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 V I Q S V T S Y T K G - - - - - D L D F T Y T S R I I V M S F P L D S V D I G F R N Q V D D I R S F L D S R H L D 101

QY 61 H Y K I V N L C A E R H Y D T A K N C R V A Q P F E D H N P P Q L E L I K P C E D L D W L S E D D N H V A I H 120
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 H Y T V N L - S P K S Y R T A K F H S R S E C S W P I R Q A P S L H N L F A V C R N Y N W L L Q N P K N V C V V H 160

QY 121 C K A G R G T G V M I C A V L L H R G F K L A Q E A L D F Y G E V R T R D K G V T I - P S O R R V V Y Y S Y L L 179
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
161 C L D G R A A S I I L G A M F I C N L Y S T G P A V - - - - - R L T Y A K R P G I G U S P H R R Y L G Y M C D L L 216

QY 180 K N H L D Y R P - V A L L F H K M F E T I M F S - G G T C N P Q F V V C Q L K V I Y S S 224
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
217 A D K - P Y R H F R E P L T I K S I T V S P V P F N K O R G C R Y C D V L I G E T K I Y T T 264

RESULT 8
YNM8 YEAST
ID YNM8 YEAST STANDARD; PRT; 434 AA.
AC P53916;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 50.2 kDa protein in CP1-SPC98 intergenic region.
GN YNL128W OR N1220 OR N1872.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Bussereau F., Jacquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MPA2,
RT MEP2, CAP/SRV2, NAM9, FKBP1/PP1/RBP1, MOM22 and CP1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.";
RL Yeast 11:1195-1209(1995).
CC -!- SIMILARITY: SOME, TO PROTEIN-TYROSINE PHOSPHATASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC or send an email to license@isb-sib.ch)
-----
```

```
-----
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; Z46843; CAA86897.1; -.
CC EMBL; Z71404; CAA96010.1; -.
CC PIR; S55155; S55155.
CC SGD; S0005072; TEPI.
CC GO; GO:0004437; F:inositol/phosphatidylinositol phosphatase a...; IDA.
CC GO; GO:0007152; P:spore wall assembly (sensu Saccharomycetes); IMP.
CC InterPro; IPR000387; TYR_phosphatase.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 434 AA; 50152 MW; E56739475D1FA898 CRC64;

Query Match 17.9%; Score 244; DB 1; Length 434;
Best Local Similarity 27.6%; Pred. No. 1.4e-15;
Matches 66; Conservative 41; Mismatches 64; Indels 68; Gaps 9;

QY 1 I I K E I V S R K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G Y V R N N I D D V V R F L D S K H N 58
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 L M K K I L S L P M K K T K N D I G L R L D I S Y I L V N L I V C S Y P V N T Y P K L Y L R N S L D D L I L F L T V Y H 81

QY 59 - K N H Y K I V N L C A E R H Y D T A K N - - - - - C R V A Q Y P F E - - - - - 88
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82 G K G N F R I F N F R G E K E D S D Y K N D L I G I A A K P E S K D F E I Q E L R S T L I N D K G I P I S I D L E T 141

QY 89 - - - - - D H N P P Q L E L I K P C E D L D W L S E D D N H V A I H C K A G K R T G 129
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
142 R T L V E E T N N V I C E R I G W L D H F P P P F E L L E I V D G I E N Y L S V S K R V A V L H C R M G K R S G 201

QY 130 V M I C A Y L L H R G F K L A Q E A L D F Y G E V R - - - - - T R D K - - - - - K G V T I P S O R R V V Y Y S Y L L 179
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
202 M I T V A Y L M - - - - - K Y L Q C P - - - - - L G E A R L I F M Q A R F K Y G M T G N G V T I P S O L R Y L R Y H E F F I 252

RESULT 9
YLPK_CABEL
ID YLPK_CABEL STANDARD; PRT; 264 AA.
AC P91301;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.3 kDa protein F46F11.3 in chromosome I.
GN F46F11.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
CC EMBL; U88173; AAK21381.1; -.
CC PIR; T25762; T25762.
CC WormPep; F46F11.3; CE10600.
KW Hypothetical protein.
FT DOMAIN 31 264
SQ SEQUENCE 264 AA; 30300 MW; 3DF3698F292BC5E5 CRC64;

Query Match 13.7%; Score 187; DB 1; Length 264;
Best Local Similarity 21.9%; Pred. No. 1.9e-10;
-----
```


RX MEDLINE=92283835; PubMed=1597462;
RA Wan J., Xu H., Grunstein M.;
RT "CDC14 of Saccharomyces cerevisiae. Cloning, sequence analysis, and
transcription during the cell cycle.";
RL J. Biol. Chem. 267:11274-11280(1992).
RN [2]
RP
RC SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
RN [3]
RP
RC SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=96287654; PubMed=8686381;
RA Eki T., Naitou M., Hagiwara H., Abe M., Ozawa M., Sasanuma S.-I.,
RA Sasanuma M., Tsuchiya Y., Shibata T., Watanabe K., Ono A.,
RA Yamazaki M.-A., Tashiro H., Hanaoka F., Murakami Y.;
RT "Fifteen open reading frames in a 30.8 kb region of the right arm of
chromosome VI from Saccharomyces cerevisiae.";
RL Yeast 12:177-190(1996).
CC -!- FUNCTION: PROBABLE PROTEIN-TYROSINE PHOSPHATASE THAT MAY BE
INVOLVED IN CHROMOSOME SEGREGATION.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.
CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN
THE N-TERMINAL DUE TO A FRAMESHIFT.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M61194; AAA34477.1; ALT_FRAME.
CC EMBL; D50617; BAA09267.1; -.
CC FIR; S56283; S56283.
CC SGD; S0001924; CDC14.
CC GO; GO:0005730; C:nucleolus; IDA.
CC GO; GO:0005816; C:spindle pole body; IDA.
CC GO; GO:0007096; P:exit from mitosis; IGI.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
CC InterPro; IPR000340; D:phosphatase.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF00782; DSPC; 1.
CC SMART; SM00195; DSPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC Cell cycle; Hydrolase.
FT ACT SITE; 283 283
FT ACT SITE; 283 283
SQ SEQUENCE 551 AA; 61906 MW; 4EB3985DFA3FD823 CRC64;
Query Match 9.5%; Score 129; DB 1; Length 551;
Best Local Similarity 26.2%; Pred. No. 0.00015;
Matches 50; Conservative 27; Mismatches 68; Indels 46; Gaps 9;
QY 7 SRNKRYQEDGFDLDLYIYNIIAMGPAER-----LEGVYRN 46
DB 166 SYKEVHEFG---DFNVLTDFIAPASQEDHPKGYLTKSSHLNQPKSVLNFANN 222
QY 47 IDDVVFLDSK--HKNHYKIYNLCARHYDTAKNCRVAQVFPEDHNPQLEIKPFCE 104
DB 223 VQLVVR-LNSHLYNKKHFDIGI---QHLDLI-----FEDGTCFDSIVKNFVGA 268
QY 105 LDQWLSEDDNHVAIHCCKAGKRGRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGT 164

DB 269 AETIKRGK--IAVCHKAGLGRGCGLGAHLIYTF-TANEICIGFLRFIR----PGMV 321
QY 165 IPSQRRVYVY 175
DB 322 VGPOQHWLYLH 332
RESULT 12
PTN8 MOUSE
ID PTN8 MOUSE STANDARD; PRT; 802 AA.
AC P293E2;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 70Z-PEP).
GN PTN8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RT "Characterization of hematopoietic intracellular protein tyrosine
phosphatases: description of a phosphatase containing an SH2 domain
and another enriched in proline-, glutamic acid-, serine-, and
threonine-rich sequences.";
RL Mol. Cell. Biol. 12:2396-2405(1992).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, LYMPH NODE, AND BONE MARROW.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M90388; AAA39394.1; -.
CC FIR; B44390; B44390.
CC PDB; 1JEG; 31-OCT-01.
CC MGD; MGI:107170; Ptpn8.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_pp.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PTPPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase; 3D-structure.
KW DOMAIN
FT ACT SITE; 227 227
FT ACT SITE; 227 227
FT ACT SITE; 227 227
SQ SEQUENCE 802 AA; 89714 MW; 0F1E45339BD4613E CRC64;
Query Match 8.8%; Score 120; DB 1; Length 802;
Best Local Similarity 32.5%; Pred. No. 0.0017;
Matches 49; Conservative 16; Mismatches 44; Indels 42; Gaps 10;
QY 57 KKHNYKIYNLCARHYDTAKNCR---VAQVPE---DHNPPQ-----LELIKPFCE 105
DB 164 KKSQDYKIRL-----KAKFNNEIRIYQHYKNWFDHVPSSIDILQLI----- 209
QY 106 DQW-----LSEDDNHVAIHCCKAGKRGRTGVMICA-----YLLHRGKFLKAQALDFYGEV 156

```
Db 210 --WDMRCYQEDDCVPCICHSAGCGRTGV-ICAVDTWMLLKDGIIIPKNFSVFNLIQEMR 266
QY 157 TRDKGVTIPSORRVYVYYSLL---KNHLD 184
Db 267 T--QRPSLVQTEQVELVYSAVLEFLFKRHMD 295

RESULT 13
VH01_RACVI
ID VH01_RACVI STANDARD; PRT; 171 AA.
AC P80994;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16) (Late
protein H1).
GN VH1.
OS Raccoon poxvirus (RCN).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10256;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93248221; PubMed=8387208;
RA Hakes D.J., Martell K.J., Zhao W.G., Massung R.F., Esposito J.J.,
RA Dixon J.E.;
RT "A protein phosphatase related to the vaccinia virus VHL is encoded
RT in the genomes of several orthopoxviruses and a baculovirus";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4017-4021(1993).
CC -!- FUNCTION: Shows activity toward tyrosine-protein phosphate as well
CC as with serine-protein phosphate.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L13165; -; NOT ANNOTATED_CDS.
CC PIR; B47452; B47452.
CC InterPro; IPR000340; DS_phosphatase.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR Pfam; PF00782; DSPC; 1.
CC DR SMART; SM00195; DSPC; 1.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
CC KW Hydrolase; Late protein.
CC FT ACT SITE 110 110 BY SIMILARITY.
CC SQ SEQUENCE 171 AA; 19741 MW; E03416F4988B3E81 CRC64;

Query Match 8.4%; Score 115; DB 1; Length 171;
Best Local Similarity 28.3%; Pred. No. 0.00073;
Matches 41; Conservative 24; Mismatches 68; Indels 12; Gaps 7;

QY 42 VYRNNDVVRFDSKHKKHYKIYNLCABRHDTAKFNCRCVQAYPEDHNPQLEIKPF 101
Db 34 VYLGNYKNAMAPSPSEKFKY-ILNLTMDK-VSFTNSNINIHPVMDTSTDISI---Y 88

QY 102 CEDLDWLGEDD--NHVAIAHCKAGKGRGTGVMICAYLLHRGKFLKAQELDF-YGEVRTR 158
Db 89 FDDITAFLEKCDORNEPVLVHCAGVNRSGAMILAYLMKSNK--ESSPMLYFLYVHSNR 146

QY 159 DKKGVTI--PSQRRVYVYYSLLKN 181
Db 147 DLRGAFVENPFSKRIIEKYVIDKN 171
```

```
RESULT 14
DUSP_VARV
ID DUSP_VARV STANDARD; PRT; 171 AA.
AC P33064;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16) (Late
protein H1).
GN H1L OR ILL.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93190624; PubMed=8383392;
RA Shchelkunov S.N., Blinov V.M., Tormenin A.V., Marennikova S.S.,
RA Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytarov V.V.,
RA Gashikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M.,
RA Andzhaparidze O.G., Sandakhchiev L.S.;
RT "Nucleotide sequence analysis of variola virus HindIII M, L, I genome
RT fragments";
RL Virus Res. 27:25-35(1993).
RN [2]
RP COMPLETE GENOME.
RX STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome";
RL Nature 366:748-751(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Garcia-1966;
RA Shchelkunov S.N., Balkin I.V., Tormenin A.V., Resenchuk S.M.,
RA Blinov V.M., Sandakhchiev L.S.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Shows activity toward tyrosine-protein phosphate as well
CC as with serine-protein phosphate.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X671119; CAA47583.1; -
CC DR EMBL; S55844; AAB24680.1; -
CC DR EMBL; X69198; CAA49025.1; -
CC DR EMBL; U22579; AAA60832.1; -
CC DR EMBL; X76264; CAA53838.1; -
CC DR PIR; B72161; B72161.
CC DR PIR; I36845; I36845.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 10, 2003, 20:29:32 ; Search time 14.1874 Seconds
(without alignments)
4529.010 Million cell updates/sec

Title: US-09-205-658A-309
Perfect score: 1362
Sequence: 1 IIKEIVSNKRYQEDGFDL.....REDKFNFFPQLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL.23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1348	99.0	403	11 O54857	O54857 rattus norv
2	1308	96.0	403	4 O43460	O43460 homo sapien
3	1294	95.0	338	4 O14781	O14781 homo sapien
4	1266	93.0	412	13 Q90XY3	Q90XY3 fugu rubrip
5	1189	87.3	402	13 Q9PUT6	Q9PUT6 xenopus lae
6	1136	83.4	369	4 Q8IVA5	Q8IVA5 homo sapien
7	695	51.0	280	11 Q8BSR7	Q8BSR7 mus musculu
8	641.5	47.1	418	5 Q9Y0B6	Q9Y0B6 drosophila
9	641.5	47.1	506	5 Q9U470	Q9U470 drosophila
10	641.5	47.1	509	5 Q9V3L4	Q9V3L4 drosophila
11	641.5	47.1	511	5 Q9Y0B5	Q9Y0B5 drosophila
12	641.5	47.1	514	5 Q9V413	Q9V413 drosophila
13	603.5	44.3	515	5 Q8T658	Q8T658 dictyosteli
14	603.5	44.3	533	5 Q8T9S7	Q8T9S7 dictyosteli
15	517	38.0	611	10 Q9LT75	Q9LT75 arabidopsis
16	517	38.0	611	10 Q8GZT8	Q8GZT8 arabidopsis

17	516	37.9	326	4 Q8WNL4	Q8WNL4 homo sapien
18	514.5	37.8	628	10 Q9SN07	Q9SN07 arabidopsis
19	514.5	37.8	632	10 Q8HI06	Q8HI06 arabidopsis
20	511	37.5	445	4 Q8WNL5	Q8WNL5 homo sapien
21	494	36.3	591	11 Q91X01	Q91X01 mus musculu
22	494	36.3	645	11 Q91X02	Q91X02 mus musculu
23	494	36.3	664	11 Q91X03	Q91X03 mus musculu
24	478	35.1	533	4 Q8NCS8	Q8NCS8 homo sapien
25	476	34.9	412	10 Q9FLZ5	Q9FLZ5 arabidopsis
26	465	34.1	962	5 O44405	O44405 caenorhabdi
27	350	25.7	1735	4 Q9HBL0	Q9HBL0 homo sapien
28	346	25.4	1715	6 Q9GLM4	Q9GLM4 bos taurus
29	340	25.0	624	11 Q8BJA7	Q8BJA7 mus musculu
30	339.5	24.9	391	4 Q8NAD0	Q8NAD0 homo sapien
31	339.5	24.9	1445	4 Q8IZW7	Q8IZW7 homo sapien
32	309	22.7	348	3 Q94526	Q94526 schizosacch
33	301.5	22.1	1285	4 Q9UPS7	Q9UPS7 homo sapien
34	301.5	22.1	1409	4 Q8NFF9	Q8NFF9 homo sapien
35	301.5	22.1	1419	4 Q8NFG0	Q8NFG0 homo sapien
36	296	21.7	398	4 Q8NV48	Q8NV48 homo sapien
37	294.5	21.6	1381	11 Q8CJ95	Q8CJ95 mus musculu
38	294.5	21.6	1400	11 Q8CGB6	Q8CGB6 mus musculu
39	282.5	20.7	222	11 Q8C6V6	Q8C6V6 mus musculu
40	271	19.9	913	4 Q75061	Q75061 homo sapien
41	246	18.1	885	11 Q8BM74	Q8BM74 mus musculu
42	212	15.6	77	4 Q9HLM7	Q9HLM7 homo sapien
43	149	10.9	1165	5 Q9VMY8	Q9VMY8 drosophila
44	129	9.5	326	3 Q05673	Q05673 saccharomyc
45	129	9.5	551	3 Q05180	Q05180 saccharomyc

ALIGNMENTS

RESULT 1

OS4857 PRELIMINARY; PRT; 403 AA.
ID O54857
AC O54857;
DC 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Protein tyrosine phosphatase and tensin homolog/mutated in multiple
DE advanced cancers protein.
GN PTEN/MMAC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Roz L., Finocchiaro G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017185; AAB96620.1; -
DR InterPro; IPR000387; TYR_PHOSPHATASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 47118 MW; 243BFE35FE209FE5 CRC64;

Query Match 99.0%; Score 1348; DB 11; Length 403;
Best Local Similarity 99.2%; Pred. No. 1.3e-124;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY	1	I I K E I V S N K R Y Q E D G F D L T Y P N I I A M G P A E R L E G V Y R N I I D V V R F L D S K H K N	60
DB	4	I I K E I V S N K R Y Q E D G F D L T Y P N I I A M G P A E R L E G V Y R N I I D V V R F L D S K H K N	63
OY	61	H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P P R E D H N P P O L E L I K P F C E D L D Q M L S E D D N V A A I H	120
DB	64	H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P P R E D H N P P O L E L I K P F C E D L D Q M L S E D D N V A A I H	123
OY	121	C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G V R T R D K R K G V T I P S Q R R Y V Y Y L L K	180

```

Db      124  CHAKGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKGVTIPSQRRYVYYSLLK 183
QY      181  NHDYRPVALLFHKKMFETIPMFSGTCNPQFVVCQKVKIYSSNSGPTREDKFNFF 240
Db      184  NHDYRPVALLFHKKMFETIPMFSGTCNPQFVVCQKVKIYSSNSGPTREDKLMYEF 243
QY      241  PQLPVCVD 249
Db      244  PQLPVCVD 252

RESULT: 2
O43460  PRELIMINARY; PRT; 403 AA.
AC O43460;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JAN-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog 2 (Fragment).
GN PTH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98127441; PubMed=9467947;
RA Kim S.K., Su L.K., Oh Y., Kemp B.L., Hong W.K., Mao L.;
RT "Alterations of PTEN/MMAC1, a candidate tumor suppressor gene, and its
RT homologue, PTH2, in small cell lung cancer cell lines.";
RL Oncogene 16:89-93 (1998).
DR EMBL; AF019083; AAC52017.1; -.
DR Genew; HGNC:9589; PTENP1.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 403 AA; 47163 MW; BDD42A4D0F26B419 CRC64;

Query Match 96.0%; Score 1308; DB 4; Length 403;
Best Local Similarity 96.8%; Pred. No. 1.1e-120;
Matches 241; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I H N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F G E V T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G I M I Y A Y L L H R G K F L K A Q E A L D F G E V T R D K G V T I P S Q R R Y V Y Y S Y L V K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F N Y F F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F M Y F F 243
QY 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 3
O14781  PRELIMINARY; PRT; 338 AA.
ID O14781;
AC O14781;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```

```

DE Hypothetical protein (Fragment).
CN PTEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99008335; PubMed=9794233;
RA Forgas E., Biesterveld E.J., Sekido Y., Fong K., Muneer S.,
RA Wistuba I.I., Milchgrub S., Brezinschek R., Virmani A., Gazdar A.F.,
RA Minna J.D.;
RT "Mutation analysis of the PTEN/MMAC1 gene in lung cancer.";
RL Oncogene 17:1557-1565 (1998).
DR EMBL; AF017999; AAB70558.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase.
FT NON_TER 1
SQ SEQUENCE 338 AA; 39899 MW; 63F3F51FBA9FA305 CRC64;

Query Match 95.0%; Score 1294; DB 4; Length 338;
Best Local Similarity 96.0%; Pred. No. 2.2e-119;
Matches 239; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I H N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F G E V T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G I M I Y A Y L L H R G K F L K A Q E A L D F G E V T R D K G V T I P S Q R R Y V Y Y S Y L V K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F N Y F F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F M Y F F 243
QY 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 4
Q90XY3  PRELIMINARY; PRT; 412 AA.
ID Q90XY3
AC Q90XY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PTEN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21455682; PubMed=11571655;
RA Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner S., Tan Y.H.,
RA Venkatesh B.;
RT "Conserved synteny between the Fugu and human PTEN locus and the
RT evolutionary conservation of vertebrate PTEN function.";
RL Oncogene 20:5554-5561 (2001).
DR EMBL; AF325922; AAL08419.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

```

```
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 412 AA; 47974 MW; 8ABEBD8B71346CE3 CRC64;

Query Match
Best Local Similarity 93.0%; Score 1266; DB 13; Length 412;
Matches 231; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 60
DB 4 I I K E V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
DB 64 H Y K I N L C A E R H Y D A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L D A Q E A L D F Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240
DB 184 N Q L E Y K P V A L L F H K M V F E T L P M F S G G T C N P Q V V V Q L K V K I H T S N P S H T R R E D K H M F E F 243
QY 241 P O P L P V C G D 249
DB 244 P O P L P V C G D 252

RESULT 5
QSPUT6
ID Q9PUT6 PRELIMINARY; PRT; 402 AA.
AC Q9PUT6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein/lipid phosphatase Pten.
GN PTEN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20021619; PubMed=1055148;
RA Lee J.O., Yang H., Georgescu M.M., Di Cristofano A., Maehama T.,
RA Shi Y., Dixon J.E., Pandolfi P., Pavletich N.P.;
RT "Crystal structure of the PTEN tumor suppressor: implications for its
RT phosphoinositide phosphatase activity and membrane association.";
RL Cell 99:323-334 (1999).
DR EMBL; AF144732; AAD46165.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 402 AA; 46878 MW; E61315E2DAB0805F CRC64;

Query Match
Best Local Similarity 87.3%; Score 1189; DB 13; Length 402;
Matches 222; Conservative 12; Mismatches 13; Indels 2; Gaps 2;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 60
DB 4 I I K E F V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
DB 64 H Y K I N L C A E R H Y D I N K F S C R V A O Y P F E D H N P P Q L E L K P F C E D L D Q L S E N E N - V A I H 122
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K 180
```

```
DB 123 C K A G K R T G V M I C A Y L L H R G K F P R A Q E A L D F Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K 182
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240
DB 183 N S L E Y R P V P L L F H K I E F E T I P M F S G G T C N P Q V V V Q L K V K I T S T A G P - K R A E K L M Y D F 241
QY 241 P O P L P V C G D 249
DB 242 P O P L P V C G D 250

RESULT 6
Q8IVAS
ID Q8IVAS PRELIMINARY; PRT; 369 AA.
AC Q8IVAS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to phosphatase and tensin homolog (Mutated in multiple
DE advanced cancers 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038293; AAH38293.1; -.
SQ SEQUENCE 369 AA; 43133 MW; 8A28D666567CD777 CRC64;

Query Match
Best Local Similarity 83.4%; Score 1136; DB 4; Length 369;
Matches 207; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 32 M G F P A E R L E G Y V R N I D D V R F L D S K H K N H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N 91
DB 1 M G F P A E R L E G Y V R N I D D V R F L D S K H K N H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N 60
QY 92 P P Q L E L K P F C E D L D W L S E D D N H V A I H C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F 151
DB 61 P P Q L E L K P F C E D L D W L S E D D N H V A I H C K A G K R T G I M I Y A Y L L H R G K F L K A Q E A L D F 120
QY 152 Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L L K N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q 211
DB 121 Y G E V R T R D K G V T I P S Q R R V Y Y Y S Y L V K N H V D Y R P V A L L F H K M F E T I P M F S G G T C N P Q 180
QY 212 F V C Q L K V K I Y S S N S G P T R R E D K F N Y P F P O P L P V C G 248
DB 181 F V C Q L K V K Y S S N S G P T R W E D K F M Y F E F P O P L P V C G 217

RESULT 7
Q8BSR7
ID Q8BSR7 PRELIMINARY; PRT; 280 AA.
AC Q8BSR7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
```

```

RL Nature 420:563-573(2002).
DR EMBL; AK030750; BAC27118.1; -.
FT NON_TER
SQ SEQUENCE 280 AA; 32522 MW; 7077A05A89ABCF2 CRC64;

Query Match
Best Local Similarity 51.0%; Score 695; DB 11; Length 280;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 CKAGKGRGTGVMTCAYLLHRRGKFLKQALDFYGEVTRDKKGVTPSQRRYYVYVYLLK 180
Db 1 CKAGKGRGTGVMTCAYLLHRRGKFLKQALDFYGEVTRDKKGVTPSQRRYYVYVYLLK 60

QY 181 NHDYRVPVALLPHKMFETIPFSGTGNPQFVWCOLKVKIYSSNGTPTREDKKNYFEF 240
Db 61 NHDYRVPVALLPHKMFETIPFSGTGNPQFVWCOLKVKIYSSNGTPTREDKKNYFEF 120

QY 241 POPLPVCGD 249
Db 121 POPLPVCGD 129

RESULT 8
QY0B6 PRELIMINARY; PRT; 418 AA.
AC QY0B6;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DE PTEN1 (EC 3.1.3.46) (CG5671-PC).
DE PTEN OR CG5671.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11;
RP SEQUENCE FROM N.A.
RA Smith A.;
RT "Alternative splicing of the Drosophila PTEN Gene.";
RN Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]

SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champs M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

```

```

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[3]

SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Dou L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]

SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]

SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]

SEQUENCE FROM N.A.
RP Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161257; AAD45362.1; -
DR EMBL; AE003628; AAN10730.1; -
DR FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
DR Hydrolase.
KW SEQUENCE 418 AA; 48066 MW; 89A6C4DDCCDAB40 CRC64;

Query Match
Best Local Similarity 47.1%; Score 641.5; DB 5; Length 418;
Matches 130; Conservative 41; Mismatches 72; Indels 17; Gaps 5;

QY 1 IIEKIVSNKRYQDGDGFDLDTIYIPNIAMGPPA-ERLGGVYRNDDVVRFLDSKHK 59
Db 11 VIRNVSVKRIYKRGYDLDLTINDNIAMGYAPDKLEGLEFRNLEDVFKLEEENHA 70

QY 60 NHYKLYNICAEHVDYTAFCNCRVQYPFEDHNPPOLEIKPCEDLDOWLSDDNNHVAAI 119
Db 71 QHYKLYNICSSERSYDAKFRGVAVYPPDDHNPPTIELIQFCSVDWMLKSSNVAV 130

QY 120 HCKAGKGRGTGVMTCAYLLHRRGKFLKQALDFYGEVTRDKKGVTPSQRRYYVYVYLL 179
Db 131 HCKAGKGRGTGVMTCAYLVFSGIKKSADALAWYDEKRTKDRKGVTPSQRRYYVYVYVYLL 190

```

Qy	180	KXHLDIRVPVALLFHKKMFETTPM	SGGTC--NPQFVVCQLKVKIYSS--NSGPT	RR---	232	
Db	191	CSVPYFSKVS	LNVCBI-----RFS	SSCVQNLGNVCSISVLHDS	ATENAKPDLKTL	244
Qy	233	---DKFN	YEFFPQPLPV	CGD	249	
Db	245	IDFQ	SKSVLTIKPS	IPVSGD	264	
RESULT 9						
ID	Q9U470	PRELIMINARY; PRT; 506 AA.				
AC	Q9U470;					
DT	01-MAY-2000	(TrEMBLrel. 13, Created)				
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)				
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)				
DE	Phosphatase and tensin homolog.					
DE	PTEN OR CG5671					
GN	Drosophila melanogaster (Fruit fly).					
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
OC	Ephydroidea; Drosophilidae; Drosophila.					
OX	NCBI_TaxID=7227;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CANTON-S;					
RX	MEDLINE=20085000; PubMed=10617573;					
RT	Goberdhan P.C.I., Paricio N., Goodman E.C., Mlodzik M., Wilson C.;					
RT	"Drosophila tumor suppressor PTEN controls cell size and number by					
RT	antagonising the Chico/PI3-kinase signalling pathway.";					
RL	Genes Dev. 13:3244-3258 (1999).					
DR	EMBL; AF201905; AAF23236.1; -.					
DR	FlyBase; FBgn0026379; Pten.					
DR	InterPro; IPR000215; Serpin.					
DR	InterPro; IPR000387; TYR phosphatase.					
DR	InterPro; IPR000242; TYR PP.					
DR	Pfam; PF00102; Y_phosphatase; 1.					
DR	PROSITE; PS00284; SERPIN; 1.					
DR	PROSITE; PS00383; TYR PHOSPHATASE_1; 1.					
DR	PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.					
KW	Hydrolase.					
SEQ	SEQUENCE 506 AA; 58128 MW; 0F64D550FFF35C36 CRC64;					
Query Match 47.1%; Score 641.5; DB 5; Length 506;						
Best Local Similarity 50.0%; Pred. No. 9.3e-55;						
Matches 130; Conservative 41; Mismatches 72; Indels 17; Gaps 5						
Qy	1	ITKEIVSRNKRKYQEDG	PDLDITYPNIIAMGRPA-ERLEGVYRN	INDVVRFLDSKH	59	
Db	11	VIRNVVSKRIYKKG	YDLDITYINDNIIAMGYAPDKJGLFRN	LEDVFKLLEENHA	70	
Qy	60	NHYKIYNLCAERHYDTAKFNCRVAQYPPEDHN	NPQLELIKPFCEDLQWLSEDDNHVAAI	119		
Db	71	QHYKIYNLCSRSYDVAKFRGVAVYV	PDNDHNPPTIELIQRFCSVDVMDLKEDSSNVAV	130		
Qy	120	HCKAGKGRGTWICAYLLHRGKFLKAQAL	DFYGEVTRDKKGVTIPSORRYVYISYLL	179		
Db	131	HCKAGKGRGTWICAYLVFSFGIKKSAD	EALAWYDEKRTKDRKGVTFIPSORRYVQYFSKL	190		
Qy	180	KXHLDIRVPVALLFHKKMFETIP	MFSGGTC--NPQFVVCQLKVKIYSS--NSGPT	RR---	232	
Db	191	CSVPYFSKVS	LNVCBI-----RFS	SSCVQNLGNVCSISVLHDS	ATENAKPDLKTL	244
Qy	233	---DKFN	YEFFPQPLPV	CGD	249	
Db	245	IDFQ	SKSVLTIKPS	IPVSGD	264	
RESULT 10						
ID	Q9V3L4	PRELIMINARY; PRT; 509 AA.				
AC	Q9V3L4; Q9U468;					

DT	01-MAY-2000	(trEMBLrel. 13, Created)
DT	01-MAY-2000	(trEMBLrel. 13, Last sequence update)
DT	01-MAR-2003	(trEMBLrel. 23, Last annotation update)
DE	Phosphatase and tensin homolog.	
GN	PTEN OR CG5671.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Berkeley;	
RX	MEDLINE=20196006; PubMed=10731132;	
RA	Adams M.D., Celisnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	
RA	Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,	
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,	
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusaker D.R., Paclob J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Sidling-Kiamos I., Sampson M., Skupski M.P., Smith T.,	
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Waasman D.A., Weinstock G.M., Weissbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	
RT	"The genome sequence of Drosophila melanogaster.;"	
RL	Science 287:2185-2195(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20011294; PubMed=10542333;	
RA	Smith A., Smith A., Alrubate S., Coelho C., Leever S.J., Ashworth A.;	
RT	Alternative splicing of the Drosophila PTEN gene.;"	
RL	Biochim. Biophys. Acta 1447:313-317(1999).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Oregon-R;	
RX	MEDLINE=20085000; PubMed=10617573;	
RA	Goberdhan D.C.I., Paricio N., Goodman E.C., Mlodzik M., Wilson C.;	
RT	"Drosophila tumor suppressor PTEN controls cell size and number by	
RT	antagonising the Chico/Pi3-kinase signaling pathway.;"	
RL	Genes Dev. 13:3244-3258(1999).	
DR	ENBL; AE003628; AAF52887.2; -	
DR	ENBL; AF161259; AAD45364.1; -	
DR	ENBL; AF201904; AAF23235.1; -	
DR	ENBL; AF201907; AAF23238.1; -	
DR	FlyBase; FBgn0026379; Pten.	
DR	InterPro; IPR000215; Serpin.	
DR	InterPro; IPR000387; Tyr phosphatase.	

```

DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase_1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
KW Hydrolase.
SQ SEQUENCE 509 AA; 58431 MW; A618527D9EFF9020 CRC64;

Query Match 47.1%; Score 641.5; DB 5; Length 509;
Best Local Similarity 50.0%; Pred.No.9.4e-55;
Matches 130; Conservative 41; Mismatches 72; Indels 17; Gaps 5;

Qy * 1 IIEKIVSRNKRKYQEDGFDLDTIYINIIAMGFPA-ERLEGVYRNIDDDVRFLDSKHK 59
Db 11 VIRNVSSKKIRIKYKEGYDLDTIYNINIIMAGYPADPKLEGLERNLEDVFKLLENHHA 70
Qy 60 NHYKIYNLCARHYDTAKFNCRVAQYFPEHDNPPOLELIKPFCDLDOWLSEDDDNHVAAI 119
Db 71 QHYKIYNLCERSVDVAKFRGRAVYFFDDHNPTIELIQFCSDVDMLKEDSNVVAV 130
Qy 120 HCKAGKGRGTGMICAYLLHRKGFLKAQDALDFYGEVTRDKKGVTIQSRRYVYYSYLL 179
Db 131 HCKAGKGRGTGMTICAYLVFSGIKKSADALAWYDEKRTKDKRGVTIPSORRYVOYFSKLV 190
Qy 180 KNLHLDYRPVALLFHKKMFETIPWFGSGTC--NPQFVVVCQLKVKIYSS--NSGPTRRE--- 232
Db 191 CSSVPYSKVSILNVCVEI-----RFSESCVQNUGMVECSVLVHDSATENAKPRLKTLTP 244
Qy 233 ---DKFNYPFFPOLPVCGD 249
Db 245 IDFKSFLVIKPSIPVSGD 264

RESULT 11
Q9YOB5 PRELIMINARY; PRT; 511 AA.
AC Q9YOB5; Q9U469;
CT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PTEN protein (EC 3.1.3.48) (Phosphatase and tensin homolog).
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RN NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Smith A.;
RT "Alternative splicing of the Drosophila PTEN Gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
[2]
SQ SEQUENCE OF 100-511 FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=20085000; PubMed=10617573;
RA Guberthan D.C.I., Particio N., Goodman E.C., Mlodzik M., Wilson C.;
RT "Drosophila tumor suppressor PTEN controls cell size and number by
antagonising the Chico/Pi3-kinase signaling pathway.";
RL Genes Dev. 13:3244-3258(1999).
DB ENBL; AF161258; AAD45363.1; -.
DB EMBL; AF201906; AAF23237.1; -.
DB FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase_1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
KW Alternative splicing; Hydrolase.
SQ SEQUENCE 511 AA; 58650 MW; 10AB4A19D3DC04D5 CRC64;
```

RESULT	13	
ID	Q8T658	
AC	PRELIMINARY;	PRT; 515 AA.
DT	08T658;	
DT	01-JUN-2002 (T-EMBLrel. 21, Created)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)	
DT	01-OCT-2002 (T-EMBLrel. 22, Last annotation update)	
DE	PTen.	
OS	Dictyostelium discoideum (Slime mold).	
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.	
OX	NCBI_TaxID=44689;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Ilijina M., Devreotes P.N.	
RT	"Dictyostelium discoideum P13 phosphatase PTEN homolog."	
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF483827; AAU9958.1;	
DR	InterPro; IPR000387; TYR_phosphatase.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE 1.	

Query Match	44.3%	Score	603.5	DB 5	Length	533	
Best Local Similarity	43.9%	Pred. No.	5.6e-51				
Matches 112; Conservative	50	Mismatches	74	Indels	19	Gaps	2
Qy	1	IKIEIVSRNRRYQEDGFDLDLTIVYPIAMGFPAPARLEGVVRKNNITDDVVRFLEDSKHN	60				
Db	4	LLRVAVSKRRYQKNGYDLDLAYITDNIAMGFPSEKVEGVFNPMKDVQRFLEDDQYHKD	63				
Qy	61	HYKIYNLCARHVDYTAFCNCRVAQYPEDNHPOLELIKPFCELDLDWLEDDNNHVAIH	120				
Db	64	HFKYNLCSERVYDHSKFGYGVYPDDNNAQFEMIDAFCRDWDAMWKEDSKNIAVIH	123				
Qy	121	CKAGKGRGTGVMICYAYLLHRGKFLKAOEALDPYGEVTRDKKGVITIPSORRYVYYSLLK	180				
Db	124	CKAGKGRGTGLMICWLMYCYGMWKNTEDSLRFYAALRTYNQKGVITIPQIRYVGVYFGSIR	183				
Qy	181	NHLIDYRPVALLFHKKMFETIP-----MFSGGTCNPFVCCOLKVKIY	222				

Db 184 ESIKVPVRNVLTKIVLRPLKPEINLSEVQFNISVGKNCVFNSEKHNMMNVWISKKKTWV 243
QY 223 SSN-SGPTREDKFN 236
Db 244 DKNKDPKPKTKTEN 258

RESULT 15

Q9LT75 PRELIMINARY; PRT; 611 AA.
AC Q9LT75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tyrosine phosphatase-like protein (Putative tyrosine
DE phosphatase).
GN AT3G19420.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Ban J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu S., Yu S., Jones L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Kawas T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen W., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene At3g19420 (GI:15230379).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025624; BAB02466.1; -
DR EMBL; AY070042; AAL49799.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00393; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 611 AA; 66430 MW; CB4FB3CFE0C6C577 CRC64;

Query Match 38.0%; Score 517; DB 10; Length 611;

Best Local Similarity 51.4%; Pred. No. 2.3e-42;

Matches 95; Conservative 31; Mismatches 51; Indels 8; Gaps 1;

QY 3 KEIVSRNERYOEDGFDLDTIYTNIIAMGPPAERL-----EGVYRNDDVVREL 54
Db 137 RHAVSQNRKRYOEGGFDLDTIYTNIIAMGPPAGDMSSGFFGYEGFYRQNMEEVINEL 196
QY 55 DSKHKHNYKIYNLCARHYDITAKFNCRVAQYPFEDHNPQLLEIKPFCELDQLWSEDDN 114
Db 197 ETQHKGYKYVNLCSERYDVSIFEGKVASFPFDDHNCPPHIVTSFCQASVWLKEDIE 256
QY 115 HVAAIHCKAGKGTGMICAYLLHKGKFLKAGALDFYGEVTRDKKGVITFSQRYVY 174
Db 257 NVVVHCKAGMARTGLMICSLLLYLKFFPTABECMDFYNQKRCVDGKGLVLPISQIRVKY 316
QY 175 VSYLL 179

Db 317 PERIL 321

Search completed: December 10, 2003, 20:34:11
Job time : 16.1874 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:11 ; Search time 61.1676 Seconds
(without alignments)
2496.336 Million cell updates/sec

Title: US-09-205-658A-310

Perfect score: 5168

Sequence: 1 MVTPPPDVSTSTRMARDL.....IAHSENFSDSNFDQAIYL 962

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5168	100.0	962	21	AA13326
2	1330	25.7	248	21	AA13324
3	508.5	9.8	430	20	AA107458
4	507.5	9.8	565	18	AAW34402
5	507	9.8	559	20	AA107456
6	507	9.8	597	20	AA107450
7	490.5	9.5	394	20	AA107457
8	490.5	9.5	403	19	AAW64784
9	490.5	9.5	403	20	AA107462

10	490.5	9.5	403	20	AA107467	Dog MMAC1 protein.
11	490.5	9.5	403	20	AA107468	Mouse MMAC1 protei
12	490.5	9.5	403	20	AA107451	Mouse tumour suppr
13	490.5	9.5	403	20	AA107444	Human tumour suppr
14	490.5	9.5	403	20	AAW97802	Dual specificity p
15	490.5	9.5	403	21	AA180119	Human PTEN protein
16	490.5	9.5	403	22	AAU08939	Human protein phos
17	490.5	9.5	403	22	AA107452	Amino acid sequenc
18	490.5	9.5	403	22	AA107452	Amino acid sequenc
19	490.5	9.5	403	23	ABP65106	Hypoxia-induced pr
20	490.5	9.5	403	23	AAE24851	Human phosphoinosi
21	490.5	9.5	403	23	AAE17879	Human PTEN protein
22	485.5	9.4	403	19	AAW64786	Human tumour suppr
23	484.5	9.4	383	19	AAW61534	Homo sapiens P-TEN
24	484.5	9.4	403	23	AAE17900	Human PTEN protein
25	482.5	9.3	403	19	AAW64785	Human tumour suppr
26	482.5	9.3	403	23	AAE17898	Human PTEN protein
27	482.5	9.3	403	23	AAE17899	Human PTEN protein
28	480.5	9.3	403	23	AAE17897	Human PTEN protein
29	465	9.0	249	21	AA133325	Caenorhabditis ele
30	442	8.6	509	22	ABB61711	Drosophila melanog
31	442	8.6	509	22	ABB66720	Drosophila melanog
32	442	8.6	514	22	ABB66721	Drosophila melanog
33	373	7.2	550	24	AAE32030	Human kinase and p
34	333.5	6.5	551	22	AAE67459	Amino acid sequenc
35	333.5	6.5	551	22	AAE67638	Amino acid sequenc
36	321	6.2	477	24	ABU07383	Human protein NOV1
37	315.5	6.1	1732	23	ABU90754	Human Tumour Endot
38	315.5	6.1	1732	24	ABU54461	Human tumour endot
39	307	5.9	508	22	ABG15911	Novel human diagno
40	298.5	5.8	523	21	AA142301	Human ORFX ORF2065
41	297.5	5.8	545	23	AAU75783	Human protein phos
42	291	5.6	385	21	AA191949	Human cytoskeleton
43	267	5.2	1561	23	ABU08170	Human cytoskeleton
44	236	4.6	85	22	ABG51931	Human liver peptid
45	236	4.6	85	22	ABG31862	Peptide #4513 enco

ALIGNMENTS

RESULT 1

AA13326
ID AA13326 standard; Protein; 962 AA.

AC AA13326;

XX
DT 12-JAN-2001 (first entry)

XX
DE Caenorhabditis elegans DAF-18.

XX
DE Caenorhabditis elegans; daf-18; insulin signalling pathway;
daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase;

KW PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes.

XX
OS Caenorhabditis elegans.

XX
FN WO200033068-A1.

XX
PD 08-JUN-2000.

XX
PF 02-DEC-1999; 99WO-US28529.

XX
PR 03-DEC-1998; 98US-0205658.

XX
PA (GEHO) GEN HOSPITAL CORP.

XX
PI Ruvkun G, Ogg S;

XX
XX WPI; 2000-423022/36.

DR
N-PSDB; AAA91623.

XX
PT Diagnosing and treating obesity and impaired glucose tolerance using

Query Match 25.7%; Score 1330; DB 21; Length 248;
 Best Local Similarity 99.2%; Pred. No. 7.6e-105;
 Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 IPTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGK 107
 DB 1 IPTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGK 60

QY 108 GNVKFNLRGGYYADNFDGNGVICFDMTDHHPSPLELMAPECREAKWLEADDDKHVIAV 167
 DB 61 GNVKFNLRGGYYADNFDGNGVICFDMTDHHPSPLELMAPECREAKWLEADDDKHVIAV 120

QY 168 HCKAGKRTGVMICALLIYINYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKL 227
 DB 121 HCKAGKRTGVMICALLIYINYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKL 180

QY 228 ERELNYLPLRMOLIGVYVERPKTWGGGSKIKEVEGNGSTILFKPDPLIISKSNHQRERA 287
 DB 181 ERELNYLPLRMOLIGVYVERPKTWGGGSKIKEVEGNGSTILFKPDPLIISKSNHQRERA 240

QY 288 TWLNCDT 295
 DB 241 TWLNCDT 248

RESULT 3
 ID AAY07458
 AC AAY07458 standard; Protein; 430 AA.
 XX AAY07458;
 DT 16-JUL-1999 (first entry)
 DE Dog TS10q23.3 gene bases 1-1290 translation product.
 KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbent assay; gene expression; dog.
 XX Canis familiaris.
 XX WO9910537-A1.
 XX 04-MAR-1999.
 XX 26-AUG-1998; 98WO-US17636.
 XX 30-APR-1998; 98US-0083563.
 XX 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 XX WPI; 1999-190638/16.
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Disclosure; Fig 9; 244pp; English.
 CC The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.

SQ Sequence 430 AA;
 Query Match 9.8%; Score 508.5; DB 20; Length 430;
 Best Local Similarity 30.3%; Pred. No. 2.3e-34;
 Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;

QY 9 PSTSTRWARDLOENPNRQCEPRVSEPYHNSIVVERIRHIFRTAVSSNRCTEYQNIIDLD 68
 DB 1 PPAARPGAACSLRRRPPRLPLSLSSFLSSHRLPDMTAAIKKEIVSRNKRKYQEDGFOLD 60

QY 69 CAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGKGVNLRGGYYADNFDG 128
 DB 61 LTYIYPNLIANGFAERLEGVYRNNDVDFLDSKL-KNHVKIYNLCAERHYDTAKFNC 119

QY 129 NVICFDMTDHHPSPLELMAPECREAKWLEADDDKHVIAHCKAGKRTGVMICALLIYIN 188
 DB 120 RVAQYPPEDHNPQLELIKPFCELDQWLSDDNHVAIHCKAGKRTGVMICAYLLHRG 179

QY 189 FYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKLREELNYLPLRMOLIGVYVERP 248
 DB 180 KFLKAQEAALDFYGEVTRDKKGVTPSORRYIYYHKLREELNYLPLRMOLIGVYVERP 239

QY 249 PKTWGGGSKIKEVEGNGSTILFKPDPLIISKSNHQRERATWLNCDTNEFDTGOKYHG 308
 DB 240 PMFSGG-----TCNPOFVVCQKVKIYSSNSGPTTR-----EDKF-- 274

QY 309 FVSKRAYCFMVPEDAPVFEVDGVRIDI--REIGLKKFSDGKIGHVWFNTMF----- 358
 DB 275 -----MYFEFPQPLPVC--GDIKVERPHKQNKMLKK--DKMFHFVWNTFFIPGPEETS 323

QY 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNRNETPMRKIDPETGNEFE 410
 DB 324 EKVENGSLCQOEIDISICIERADNDKEYL-----VLTLTKNDLQKANKKANKRYF 373

QY 411 SP 412
 DB 374 SP 375

RESULT 4
 AAW34402
 ID AAW34402 standard; Protein; 565 AA.
 XX AAW34402;
 AC AAW34402;
 DT 06-MAR-1998 (first entry)
 DE Protein encoded by gene of IMAGE clone 264611.
 KW IMAGE clone 264611; gene fragment; human; chromosome 10; D10S541 marker;
 KW D10S215 marker; tumour suppressor gene; prostatic cancer; cancer therapy;
 KW melanoma; glioma; non-Hodgkin's lymphoma; cancer susceptibility;
 KW diagnosis; prognosis; mutation detection; suppressor gene; neoplasia;
 KW hyperplasia; 10q loss tumour.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 484
 FT /label= unknown
 FT /note= "encoded by RAA"
 XX
 PN WO9715686-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 22-OCT-1996; 96WO-GB02588.
 XX
 PR 23-OCT-1995; 95US-0005840.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Gray IC, Spurr NK;

XX WPI: 1997-259037/23.
 DR N-PSDB; AAT93354.
 XX
 PT Nucleic acid hybridizing to chromosome 10 tumour suppressor gene -
 PT useful for diagnosis, prognosis and treatment of prostatic cancer
 PT and for assessing susceptibility to cancer
 XX
 PS Claim 20; Fig 7; 127pp; English.
 XX
 CC This sequence represents the protein encoded by the cDNA of the gene
 CC from the IMAGE clone 264611. The cDNA sequence, and the sequences of its
 CC exons (see AAT93326-793333) are all nucleic acid sequences of the
 CC invention. The nucleic acid of the invention (I) is able to hybridise
 CC selectively to the region of human chromosome 10 bounded by the markers
 CC D10S41 and D10S215. (I) is a tumour suppressor gene, particularly
 CC involved in prostatic cancer but also in melanoma, glioma and
 CC rbn-Hodgkin's lymphoma. Any nucleic acid that hybridises selectively to
 CC the specified chromosomal region can be used to determine susceptibility
 CC of a patient to cancer and for diagnosis/prognosis, especially of
 CC prostatic cancer, i.e. by detecting mutations. The wild-type suppressor
 CC gene can also be used to treat cancer, especially when included in a
 CC viral vector. Similar detection methods can be based on the amount of
 CC protein encoded by (I), or its truncation or loss, in a sample,
 CC particularly using labelled molecules capable of hybridising to the
 CC protein, particularly antibodies. The labelled molecules when coupled to
 CC a cytotoxin can be used for cancer treatment. The encoded protein can be
 CC used to raise antibodies and these used to screen DNA expression
 CC libraries or for polypeptide isolation. (I) allows differential diagnosis
 CC between neoplasia and hyperplasia of the prostate (all tumours with a 10q
 CC loss have lost this region) and determination of micro-metastases in the
 CC blood.
 XX
 SQ Sequence 565 AA;
 Query Match 9.8%; Score 507.5; DB 18; Length 565;
 Best Local Similarity 31.2%; Pred. No. 4.4e-34;
 Matches 130; Conservative 66; Mismatches 159; Indels. 61; Gaps 11;
 QY 10 STSTRSMARD-LOENPNRQGPBPVSEPHNSIVERIRHIFRTAVSSNRCRTEYQNDLD 68
 DB 127 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTALIKEIVSRNKRKYQDGFDD 186
 QY 69 CAYITDRIIAGYATGIEANFRNSKVQOFLTRRHGKGNVFNLRGGYYDADNPDG 128
 DB 187 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCARHYDTAKENC 245
 QY 129 NVICFDMTDHPPSLEMAPFCREAKEWLEADKHVIAVHCAGKGRGTGMICALLIYN 188
 DB 246 RVAQYPPFDHNPQLEIKPFCELDQWLSDDNHVAAIHCHAGKGRGTGMICALLHRG 305
 QY 189 FVPSRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
 DB 306 KFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 365
 QY 249 PKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQBERATWLNCDTNEPFTGQKYHG 308
 DB 366 PMFSGG-----TCNPQFVVCQKLVKIISSNSGPTTR-----EDKF-- 400
 QY 309 FVSKRAYCFWVPEDAPVFEVDVIRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 DB 401 -----MYFEFPQPLPVC--GDIKVEFFHKQNKMLK---DKMFHFWNTTFFIPGPEETS 449
 QY 359 -----ACDGLNG-GHFEYVDKTPYI-----GDDTSIGRKNMGRNETPMRKI 401
 DB 450 EKVENGLCQDIBDSICSIERADNDKEYLVLTXTNLDLKDANKDKANRYFSPNFV 505
 RESULT 5
 AAY07456
 ID AAY07456 standard; peptide; 559 AA.
 XX
 AC AAY07456;

XX 16-JUL-1999 (first entry)
 DT Mouse TS10q23.3 gene bases 283-1959 translation product.
 XX
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; mouse.
 XX
 OS Mus musculus.
 XX
 XX WO9910537-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 26-AUG-1998; 98WO-US17636.
 XX
 PR 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 XX
 DR WPI; 1999-190638/16.
 XX
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX
 PS Disclosure; Fig 9; 244pp; English.
 XX
 CC The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX
 SQ Sequence 559 AA;
 Query Match 9.8%; Score 507; DB 20; Length 559;
 Best Local Similarity 30.6%; Pred. No. 4.7e-34;
 Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;
 QY 10 STSTRSMARD-LOENPNRQGPBPVSEPHNSIVERIRHIFRTAVSSNRCRTEYQNDLD 68
 DB 121 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTALIKEIVSRNKRKYQDGFDD 180
 QY 69 CAYITDRIIAGYATGIEANFRNSKVQOFLTRRHGKGNVFNLRGGYYDADNPDG 128
 DB 181 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCARHYDTAKENC 239
 QY 129 NVICFDMTDHPPSLEMAPFCREAKEWLEADKHVIAVHCAGKGRGTGMICALLIYN 188
 DB 240 RVAQYPPFDHNPQLEIKPFCELDQWLSDDNHVAAIHCHAGKGRGTGMICALLHRG 299
 QY 189 FVPSRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
 DB 300 KFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 359
 QY 249 PKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQBERATWLNCDTNEPFTGQKYHG 308
 DB 360 PMFSGG-----TCNPQFVVCQKLVKIISSNSGPTTR-----EDKF-- 394
 QY 309 FVSKRAYCFWVPEDAPVFEVDVIRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 DB 395 -----MYFEFPQPLPVC--GDIKVEFFHKQNKMLK---DKMFHFWNTTFFIPGPEETS 443
 QY 359 -----ACDGLNG-GHFEYVDKTPYI-----GDDTSIGRKNMGRNETPMRKIDPBTGNEFE 410

```
Db 444 EKVENSLCDQDEIDSICSIERADNDKEYL-----VLTLTKNLDKANKOKANRYF 493
QY 411 SP 412
Db 494 SP 495

RESULT 6
ID AAY07450
XX AAY07450 standard; peptide; 597 AA.
XX AAY07450;
XX 16-JUL-1999 (first entry)
XX Human TS10q23.3 gene bases 453-2243 translation product.
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
XX Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX enzyme linked immunosorbant assay; gene expression; human.
XX Homo sapiens.
XX OS
XX PN WO9910537-A1.
XX PD 04-MAR-1999.
XX PF 26-AUG-1998; 98WO-US17636.
XX PR 30-APR-1998; 98US-0083563.
XX PR 26-AUG-1997; 97US-0057750.
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
XX PI Yung WKA;
XX DR WPI; 1999-190638/16.
XX PT Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
XX PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
XX PT Syndrome and susceptibility to breast cancer
XX PS Disclosure; Fig 9; 244pp; English.
XX CC The invention relates to mutant genes encoding the tumour suppressor
XX CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
XX CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
XX CC gland and endometrium (claimed). The mutant gene is also useful for
XX CC diagnosing a subject who has a predisposition to breast cancer. Both
XX CC methods involve antibodies, which specifically bind to a TS10q23.3,
XX CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX SQ Sequence 597 AA;
XX Query Match 9.8%; Score 507; DB 20; Length 597;
XX Best Local Similarity 30.6%; Pred. No. 5.2e-34;
XX Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTRSMARD-LQENPNRQGEPRVSEPYHNSIGVERIRHIFRTAVSSNRCRTEYQNIIDL 68
Db 159 SATAKSRAISILQKPRHQQLPSLSFFFSFHLRDPMTALIKEIVSNKRKRRYQEDGFDLD 218
QY 69 CAYITDRIIAGYPATGIEANFRNSKVQOQLTRRHGKGNVKNLRCGGYYVDADNPDG 128
Db 219 LTYIYFNIIAMGPAERLEGVYRNNDIVVRELDKSH-KNHYKIVNLCRAERYHTAKENC 277
QY 129 NVICDMTDHPPSLMELAPFCREKLEADKKVIAVHCKAGKGRGTGVMICALLIYN 188
Db 278 RVAQYPFEDHNPQELIKPFCELDQWLSUEDDNHVAIHCAGKGRGTGVMICAYLLHRG 337
```

```
QY 189 FYPSPROILDYYSIIRTKNNKGVITIPSORRYVYYHKLREBELNYLPLRMQLIGVYVERP 248
Db 338 KFLQAQEAALDFYGEVTRDRKKGVTIPSORRYVYYSYLLKKNHLDYRPPVALLFHQOMFETI 397
QY 249 PKTWGGGSKI KVEVEGNGSTILFKPDPLIISKNHQRERATWLNNCDTNEFDTGQKYHG 308
Db 398 PMFSGG-----TCNPQFVVQQLVKIYSSNSGPTTR-----EDKF-- 432
QY 309 FVSKRAYCFMVPEDAPVFEVDVRI--REIGFLKKFSDGKI GHVWNTWTF----- 358
Db 433 -----MYFEPQPLPVC--GDIKVEFFHKQKMLKK--DKMFHFVWNTFFIPGPEETS 481
QY 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNGRNRNETPMRKIDPETGNEFE 410
Db 482 EKVENSLCDQDEIDSICSIERADNDKEYL-----VLTLTKNLDKANKOKANRYF 531
QY 411 SP 412
Db 532 SP 533

RESULT 7
ID AAY07457
XX AAY07457 standard; Protein; 394 AA.
XX AC AAY07457;
XX DT 16-JUL-1999 (first entry)
XX DE Dog tumour suppressor protein TS10q23.3.
XX KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
XX KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX KW enzyme linked immunosorbant assay; gene expression; dog.
XX OS Canis familiaris.
XX PN WO9910537-A1.
XX PD 04-MAR-1999.
XX PF 26-AUG-1998; 98WO-US17636.
XX PR 30-APR-1998; 98US-0083563.
XX PR 26-AUG-1997; 97US-0057750.
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
XX PI Yung WKA;
XX DR WPI; 1999-190638/16.
XX DR N-PSDB; AAX57673.
XX PT Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
XX PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
XX PT Syndrome and susceptibility to breast cancer
XX PS Disclosure; Fig 9; 244pp; English.
XX CC The invention relates to mutant genes encoding the tumour suppressor
XX CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
XX CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
XX CC gland and endometrium (claimed). The mutant gene is also useful for
XX CC diagnosing a subject who has a predisposition to breast cancer. Both
XX CC methods involve antibodies, which specifically bind to a TS10q23.3,
XX CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX SQ Sequence 394 AA;
XX Query Match 9.5%; Score 490.5; DB 20; Length 394;
XX Best Local Similarity 31.3%; Pred. No. 7e-33;
```

Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTERRHCK 107

Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H - K 62

QY 108 G N V K F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E L M A P F C R E A K E W L E A D D K H V I A V 167

Db 63 N H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R O I L D Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227

Db 123 H C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287

Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G L K K F S 345

Db 235 - - - - - E D K F - - - - - M Y F E F P Q P L P V C - - G D I K V E F F H K N K M L K - - 267

QY 346 D K I G H V W F N T M F - - - - - A C D G L N G - G H F E Y V D K T O P Y I G D D T S I G R K N 389

Db 268 - D K M F H F W N T F F I P G P E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L - - - - - 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412

Db 317 V L T L T K N D L D K A N K D K A N Y F S P 339

RESULT 8

AAW64784

ID AAW64784 standard; Protein; 403 AA.

XX

AC AAW64784;

XX

DT 03-NOV-1998 (first entry)

XX

DE Human tumour suppressor TS10q23.3 protein.

XX

KW Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;

KW brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;

KW drug screening.

XX

OS Homo sapiens.

XX

PN WO9833907-Al.

XX

PD 06-AUG-1998.

XX

PF 08-JAN-1998; 98WO-US00353.

XX

PR 30-JAN-1997; 97US-0791115.

XX

PA (MYRI-) MYRIAD GENETICS INC.

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;

PI Yung WKA;

XX

DR WPI; 1998-437461/37.

DR N-PSDB; AAW46392.

XX

XX Tumour suppressor TS10q23.3 and related antibodies - useful for

PT diagnosis, staging and treatment of cancer, especially of breast,

PT prostate and brain

XX

PS Claim 1; Fig 7; 161pp; English.

XX

CC This sequence represents the human tumour suppressor protein TS10q23.3.

CC This protein can be used to diagnose a wide range of tumours,

CC particularly of prostate, breast and brain (glioma), to stage cancers

CC (particularly differentiation between low grade brain cancer and glioma)

CC and for prediction of metastasis. This suppressor and its nucleic acid

CC are also used to alter the phenotype to specifically treat cancer cells,

CC e.g. by in vivo or ex vivo gene therapy, optionally together with other

CC anti-cancer agents. Fragments of the suppressor can be coupled to an

CC immunogenic carrier and are used to raise antibodies, to isolate

CC antigens, as immunoassay reagents, to clone related DNA or for

CC immunotherapy. Antisense nucleic acid can be used to produce transgenic

CC animals (useful for drug screening) or to eliminate dominant negative

CC mutants.

XX

SQ Sequence 403 AA;

Query Match 9.5%; Score 490.5; DB 19; Length 403;

Best Local Similarity 31.3%; Pred. No. 7.2e-33;

Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTERRHCK 107

Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H - K 62

QY 108 G N V K F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E L M A P F C R E A K E W L E A D D K H V I A V 167

Db 63 N H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R O I L D Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227

Db 123 H C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287

Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G L K K F S 345

Db 235 - - - - - E D K F - - - - - M Y F E F P Q P L P V C - - G D I K V E F F H K N K M L K - - 267

QY 346 D K I G H V W F N T M F - - - - - A C D G L N G - G H F E Y V D K T O P Y I G D D T S I G R K N 389

Db 268 - D K M F H F W N T F F I P G P E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L - - - - - 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412

Db 317 V L T L T K N D L D K A N K D K A N Y F S P 339

RESULT 9

AAW07462

ID AAW07462 standard; peptide; 403 AA.

XX

AC AAW07462;

XX

DT 16-JUL-1999 (first entry)

XX

DE Mouse MMAC1 protein sequence.

XX

KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;

KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;

KW enzyme linked immunosorbant assay; gene expression; mouse.

XX

OS Mus musculus.

XX

PN WO9910537-Al.

XX

PD 04-MAR-1999.

XX

PF 26-AUG-1998; 98WO-US17636.

XX

PR 30-APR-1998; 98US-0083563.

PR 26-AUG-1997; 97US-0057750.

XX

PA (MYRI-) MYRIAD GENETICS INC.

PA (TEXA) UNIV TEXAS SYSTEM.


```

DE Mouse MMAC1 protein.
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX enzyme linked immunosorbant assay; gene expression; mouse.
OS Mus musculus.
XX WO9910537-A1.
XX 04-MAR-1999.
XX *26-AUG-1998; 98WO-US17636.
XX 30-APR-1998; 98US-0083563.
PR 26-AUG-1997; 97US-0057750.
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX WPI; 1999-190638/16.
DR N-PSDB; AAX57700.
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PT Syndrome and susceptibility to breast cancer
XX Disclosure; Page 236-238; 244pp; English.
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX Sequence 403 AA;

Query Match 9.5%; Score 490.5; DB 20; Length 403;
Best Local Similarity 31.3%; Pred. No. 7.2e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGCIANFRNSKVQTOQFLTRRHGK 107
DB 4 IIKKIVSRNKRKYQEDGFDLDLTYYIPNIIANGFPAERLEGVYRNNDVVRFDSKH-K 62
QY 108 GNVKVNLRGGYYDADNFDGNVICFDMTDHPPSLELMAPFCREAKEWLEADDKHVIAV 167
DB 63 NHYKIYNLCARHYDTAKFNCRVAQYPPFDHNPQLEIKPFCELDQWLSDDNHVAAI 122
QY 168 HCKAGKGRGTGMICALLIYINFPSPRQILDYYSIIRTKNNKGVITIPSORRYIYYHKL 227
DB 123 HCKAGKGRGTGMICAYLLHRGKFLKAQEBALDFYGEVTRDKKGVITIPSORRYIYYSYLL 182
QY 228 ERELNYLPLRMQLIGVYVERPPTKGGGSKI KVEVNGNSTILFKPDPPLIISKSNHQRERA 287
DB 183 KNLHDYRPVALLFHKKMFETIPMFSGG-----TCNPQFVVQQLKVKIYSSNGPTRR- 234
QY 288 TWLNCDTNEFDTEGQKYHGFVSKRAYCFMVPEADPVFVEGDVRIDI--REIGFLKKFS 345
DB 235 -----EDKP-----MYFEFPQPLPVC--GDIKVEFFHKQMKLKK-- 267
QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEVVDKTOPYIGDTSIGRKN 389
DB 268 -DKMFHWNTWFIPGPETSEKVENGLCDQEISIERADNDKEYL----- 316
QY 390 GMRNETPMRKIDPETGNFEFSP 412
DB 317 VLTLTKNLDLKANKDKANRYFSP 339

```

Db 235 -----EDKF-----MYFFPQLPVC--GDIVKVEFFHKNKMLKK-- 267
AY07444
Qy 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316
Qy 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDKANKKANRYFSP 339
RESULT 13
ID AAY07444 standard; Protein; 403 AA.
AC AAY07444;
XX
DT 16-JUL-1999 (first entry)
XX
DE Human tumour suppressor protein TS10q23.3.
XX
KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW enzyme linked immunosorbent assay; gene expression; human.
XX
OS Homo sapiens.
XX
PN WO9910537-A1.
XX
PD 04-MAR-1999.
XX
PF 26-AUG-1998; 98WO-US17636.
XX
PR 30-APR-1998; 98US-0083563.
PR 26-AUG-1997; 97US-0057750.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX
DR WPI; 1999-190638/16.
DR N-PSDB; AAX57671.
XX
PT Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PT Syndrome and susceptibility to breast cancer
XX
PS Disclosure; Fig 7; 244pp; English.
XX
CC The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3.
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX
SQ Sequence 403 AA;
Query Match 9.5%; Score 490.5; DB 20; Length 403;
Best Local Similarity 31.3%; Pred. No. 7.2e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
Qy 48 IFTAVSSNRCRTEYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVTOQFLRRHGK 107
Db 4 IIEIVSRNKRKYQEDGFDLTYIYPNIAMGFAERLEGVYRNIDVVRFLDSKH-K 62
Qy 108 GNVKVPNLRGGYYDADNPDGNCVCFDTHDHPSPLELMAPPCKRAKWLADKHVIAV 167
Db 63 NHYKIYNLCAERHYHTAKFNCRVAQYPPEDHNPPQLELIKPFCDLDQWLSDDDNHAAI 122

Qy 168 HCKAGKGRGVMICALLIYINFPSPRQILDYVSIIRTKNNKGVITPSQRRIYYHKLK 227
Db 123 HCKAGKGRGVMICAYLLHRGKFLKAQEAFLDGEVTRDKKGVITPSQRRIYYVSYLL 182
Qy 228 ERELNYLPLRMQLIGVVVERPKTWGGSKIKVEVGNGSTILFKPDPDLIISSKNHQRERA 287
Db 183 KNLIDYRFPVALLFHMMFETIPMFSGG-----TCNPFQVVCQKVKIYSSNGPTRR- 234
Qy 288 TLLNCDTPNEFDTEQKYHGFVSKRAYCFMVPEADPVFVGDVIRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFFPQLPVC--GDIVKVEFFHKNKMLKK-- 267
Qy 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316
Qy 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDKANKKANRYFSP 339
RESULT 14
ID AAW97802 standard; Protein; 403 AA.
AC AAW97802;
XX
DT 21-MAY-1999 (first entry)
XX
DE Dual specificity phosphatase PTEN.
XX
KW PTEN; MMAC1; protein tyrosine phosphatase; human; prostate cancer;
KW brain cancer; prostate cancer; tumour suppressor; Cowden's disease;
KW neurodegenerative disease; Parkinson's disease; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9902704-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-US14205.
XX
PR 29-JUN-1998; 98US-0090984.
PR 08-JUL-1997; 97US-0051908.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Myers MP, Tonks NK;
XX
DR WPI; 1999-120905/10.
DR N-PSDB; AAX07339.
XX
PT New use of PTEN phosphatase - for developing products for the
PT diagnosis and treatment of hyperproliferative disorders, e.g.
PT cancers or neurodegenerative disorders such as Parkinson's disease
XX
PS Disclosure; Fig 1A-C; 60pp; English.
XX
CC This is the amino acid sequence of human PTEN phosphatase,
CC predicted from the PTEN gene (see AAX07339) located at 10q22-23.
CC PTEN shares homology with the protein tyrosine phosphatase in
CC family. It can function as a dual specificity phosphatase in
CC vitro, displaying selectivity for extremely acidic substrates.
CC PTEN dephosphorylates phosphatidylinositol in vitro, and displays
CC selectivity for the 3 position of the inositol ring. It is also
CC able to dephosphorylate serine, threonine and tyrosine residues
CC when present in acidic substrates. The phosphatase activity of
CC PTEN is required for its ability to function as a tumour suppressor
CC or an apoptosis inducer. Point mutations, including point mutations
CC in tumour samples and Cowden's disease kindreds, ablate PTEN
CC activity. PTEN functions as an upstream, negative regulator of

CC PKB/Akt and has the potential to regulate signals associated with
 CC control of cell survival. PTEN polypeptides and polynucleotides
 CC can be used in the diagnosis and treatment of conditions
 CC characterised by an alteration in PTEN which causes an alteration
 CC of phosphatase activity. They can be used to treat
 CC hyperproliferative conditions such as cancers, e.g. brain, prostate
 CC or breast cancers or Cowden's disease, or other hyperproliferative
 CC diseases involving reduced phosphatase activity. They can also be
 CC used in methods of reducing PTEN phosphatase activity for treating
 CC conditions such as Parkinson's disease and other neurodegenerative
 CC disease.
 XX
 XX
 SQ *Sequence 403 AA;
 Query Match 9.5%; Score 490.5; DB 20; Length 403;
 Best Local Similarity 31.3%; Pred. No. 7.2e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFTAVSSNRCTEQYQNDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
 DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62
 QY 108 G N V K V N L R G G Y Y D A N D N G V I C F D M T D H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167
 DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A I 122
 QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y S I I R T K N K G V T I P S O R R Y I Y Y H K L R 227
 DB 123 H C K A G K G R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182
 QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287
 DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G ----- T C N P Q F V V C Q L K V I Y S N S G P T R R - 234
 QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G L K K F S 345
 DB 235 ----- E D K F ----- M Y F E F P Q P L P V C - - G D I K V E F F H K Q N K M L K K - - 267
 QY 346 D G K I G H V W F N T M F ----- A C D G G L N G - G H F E Y V D K T Q P Y I G D D T S I G R K N 389
 DB 268 - D K M F H F W N T F F I P G P E E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L ----- 316
 QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
 DB 317 V L T L T K N D L D K A N K A N R Y F S P 339
 RESULT 15
 AAY80119
 ID AAY80119 standard; Protein; 403 AA.
 AC AAY80119;
 XX
 XX 22-MAY-2000 (first entry)
 XX
 XX Human PTEN protein sequence SEQ ID NO:1.
 XX
 XX Human; PTEN; MMAC1; TEPI; phosphorothioate; antisense oligonucleotide;
 KW inhibition; protein phosphatase; tumour; diagnosis; inflammation;
 KW anticancer; anti-inflammatory; anti-infective; infection.
 XX
 OS Homo sapiens.
 XX
 XX US6020199-A.
 XX
 XX 01-FEB-2000.
 XX
 XX 21-JUL-1999; 99US-0358381.
 XX
 XX 21-JUL-1999; 99US-0358381.
 XX
 XX (ISIS-) ISIS PHARM INC.

PI Monia BP, Cowser LM;
 XX
 XX WPI; 2000-181363/16.
 DR N-PSDB; AA291361.
 XX
 PT New antisense compounds useful for treating, preventing or diagnosing
 PT e.g. tumors or inflammation, are targeted to the human dual specificity
 PT protein phosphatase (PTEN) sequence -
 XX
 XX Claim 1; Column 43-46; 32pp; English.
 XX
 CC The present invention describes phosphorothioate antisense
 CC oligonucleotides that are targeted to the 3'-untranslated region (UTR)
 CC of the sequence encoding a human dual specificity protein phosphatase
 CC designated PTEN (also known as MMAC1 and TEPI), and hybridise
 CC specifically to the human PTEN nucleotide sequence given in AA291361.
 CC The antisense oligonucleotides have anticancer, anti-inflammatory and
 CC anti-infective activities. The phosphorothioate antisense
 CC oligonucleotides can be used for diagnosis, treatment and prevention of
 CC PTEN-related diseases, e.g. infections, inflammation and tumours.
 CC The present sequence represents the human PTEN protein sequence.
 XX
 XX Sequence 403 AA;
 Query Match 9.5%; Score 490.5; DB 21; Length 403;
 Best Local Similarity 31.3%; Pred. No. 7.2e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFTAVSSNRCTEQYQNDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
 DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62
 QY 108 G N V K V N L R G G Y Y D A N D N G V I C F D M T D H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167
 DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A I 122
 QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y S I I R T K N K G V T I P S O R R Y I Y Y H K L R 227
 DB 123 H C K A G K G R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182
 QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287
 DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G ----- T C N P Q F V V C Q L K V I Y S N S G P T R R - 234
 QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G L K K F S 345
 DB 235 ----- E D K F ----- M Y F E F P Q P L P V C - - G D I K V E F F H K Q N K M L K K - - 267
 QY 346 D G K I G H V W F N T M F ----- A C D G G L N G - G H F E Y V D K T Q P Y I G D D T S I G R K N 389
 DB 268 - D K M F H F W N T F F I P G P E E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L ----- 316
 QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
 DB 317 V L T L T K N D L D K A N K A N R Y F S P 339
 Search completed: December 10, 2003, 20:32:16
 Job time : 62.1676 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:47 ; Search time 23.8315 Seconds
(without alignments)
1707.948 Million cell updates/sec

Title: US-09-205-658A-310

Perfect score: 5168

Sequence: 1 MVTPPPDPVPTSTRMARDL.....IAHSENFSDSNFDQAIYL 962

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap:**
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508.5	9.8	430	3	US-08-791-115B-7
2	508.5	9.8	430	3	US-09-140-749-18
3	507.5	9.8	565	3	US-08-906-156A-12
4	507	9.8	559	4	US-09-140-749-15
5	507	9.8	597	4	US-09-140-749-8
6	507	9.8	645	3	US-08-791-115B-6
7	507	9.8	742	3	US-08-791-115B-5
8	490.5	9.5	394	3	US-08-791-115B-27
9	490.5	9.5	394	4	US-09-140-749-17
10	490.5	9.5	403	3	US-08-791-115B-1
11	490.5	9.5	403	3	US-08-791-115B-23
12	490.5	9.5	403	3	US-08-791-115B-25
13	490.5	9.5	403	4	US-09-140-749-2
14	490.5	9.5	403	4	US-09-140-749-10
15	490.5	9.5	403	4	US-09-140-749-49
16	490.5	9.5	403	4	US-09-140-749-55
17	490.5	9.5	403	4	US-09-140-749-57
18	152	2.9	783	6	5231168-2
19	137.5	2.7	1177	4	US-09-134-001C-5106
20	136	2.6	1053	4	US-09-394-272-6
21	133.5	2.6	1054	1	US-08-356-354-4
22	133.5	2.6	1054	2	US-08-778-656-4
23	133.5	2.5	1054	1	US-09-394-272-3
24	130.5	2.5	1852	1	US-08-425-061-24
25	130.5	2.5	1852	2	US-08-825-886-24
26	130.5	2.5	1852	4	US-08-989-890-24
27	130.5	2.5	1863	1	US-08-425-061-16

28 130.5 2.5 1863 1 US-08-480-784-2
29 130.5 2.5 1863 1 US-08-483-553-2
30 130.5 2.5 1863 1 US-08-487-002-2
31 130.5 2.5 1863 1 US-08-483-554B-2
32 130.5 2.5 1863 1 US-08-488-011B-2
33 130.5 2.5 1863 2 US-08-825-886-16
34 130.5 2.5 1863 2 US-08-603-753D-2
35 130.5 2.5 1863 3 US-09-099-753-2
36 130.5 2.5 1863 3 US-08-850-727-2
37 130.5 2.5 1863 3 US-08-986-106-2
38 130.5 2.5 1863 4 US-09-007-678B-49
39 130.5 2.5 1863 4 US-08-989-890-16
40 130.5 2.5 1863 5 PCT-US95-10202-2
41 130.5 2.5 1863 5 PCT-US95-10203-2
42 130.5 2.5 1863 5 PCT-US95-10220-2
43 126.5 2.4 1579 3 US-08-755-587-184
44 126.5 2.4 1863 1 US-08-798-691-4
45 126.5 2.4 1863 3 US-08-825-487A-4

ALIGNMENTS

RESULT 1
US-08-791-115B-7
; Sequence 7, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rohmwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08791.115B
; APPLICATION NUMBER: US/08791.115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-791-115B-7
Query Match 9.8%; Score 508.5; DB 3; Length 430;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;

QY 9 PSTSTRMARDLQENRQCPGPRVSPYHNSIVERTHIFRTAVSSNRCTEQNDLDD 68

DB 1 PPAARPGAACSLRRRRPRRPLLLSLSLSHRLPDMTATIKETVSRNKRKYQEDGFDLD 60

QY 69 CAVITDRITAIAGVPATGIEANERNKSVQOQLTRHGGKGVNLRGGYVYDADNPDG 128
 Db 61 LTYIYPIIANGPFAERLSEGVYRNNDVVRELDKSH-KNHYKIYNLCARHYDTAKFNC 119
 QY 129 NVICFDMTDHPPSLMELAPFCREAKEWLEADKHVIAVHCAGKAGRTGVMICALLIYN 188
 Db 120 RVAQYFPEDHNPQLEIKPFCELDLWLSSEDDNHVAALHCAGKAGRTGVMICAYLLHRG 179
 QY 189 FVSPRQILDYYSIIRTKNKGVTIPSORRYIYVYHKLREELNVLPLRMQLIGVYVERP 248
 Db 180 KFLKAQEAALDFYGEVTRDKKGVITIPSORRYIYVYHKLREELNVLPLRMQLIGVYVERP 239
 QY 249 PKTWGGGSKIKEVEGNGSTILFKPDPLIISKNHQRERATWLNNCDTNEPDTGQKYHG 308
 Db 240 PMFSGG-----TCNPOFVVQOLKVKIYSSNSGPTRR-----EDKF-- 274
 QY 309 FVSKRAYCFMVPEDAPVVEGDVRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 Db 275 -----MYFEFQPLPVC--GDIKVEFFHKQKMLKK---DKMFHFVWNTTFFIPGPEETS 323
 QY 359 -----ACDGLNG-GHFEYVDKTOPYIGDDTSIGRKNGMRRNETPMRKIDPETGNEFE 410
 Db 324 EKVENGLCDQBIIDSICSTERADNDKEYL-----VLTLTKNLDLKDANKKANKRYF 373
 QY 411 SP 412
 Db 374 SP 375

RESULT 2

US-09-140-749-18
 ; Sequence 18, Application US/09140749
 ; Patent No. 6482795
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, Alfred W.K.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; FILE REFERENCE: 2318-205
 ; CURRENT APPLICATION NUMBER: US/09/140,749
 ; EARLIER FILING DATE: 1998-08-26
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER APPLICATION NUMBER: U.S. 60/057,750
 ; EARLIER FILING DATE: 1997-08-26
 ; EARLIER APPLICATION NUMBER: U.S. 60/083,563
 ; EARLIER FILING DATE: 1998-04-30
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-09-140-749-18

Query Match 9.8%; Score 508.5; DB 4; Length 430;
 Best Local Similarity 30.3%; Pred. No. 1.5e-34;
 Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;

QY 9 PSTSTRMARDLOENPNRQGEPRVSEPYHNSIVERIRHIFRTAVSSNCRTEYQNIIDL 68
 Db 1 PPAARPGACSLRRRRPPLPSLSFLSSHLRDPMTAIKEIVSRNRRRYQEDGFOLD 60
 QY 69 CAVITDRITAIAGVPATGIEANERNKSVQOQLTRHGGKGVNLRGGYVYDADNPDG 128
 Db 61 LTYIYPIIANGPFAERLSEGVYRNNDVVRELDKSH-KNHYKIYNLCARHYDTAKFNC 119
 QY 129 NVICFDMTDHPPSLMELAPFCREAKEWLEADKHVIAVHCAGKAGRTGVMICALLIYN 188
 Db 120 RVAQYFPEDHNPQLEIKPFCELDLWLSSEDDNHVAALHCAGKAGRTGVMICAYLLHRG 179

QY 189 FVSPRQILDYYSIIRTKNKGVTIPSORRYIYVYHKLREELNVLPLRMQLIGVYVERP 248
 Db 180 KFLKAQEAALDFYGEVTRDKKGVITIPSORRYIYVYHKLREELNVLPLRMQLIGVYVERP 239
 QY 249 PKTWGGGSKIKEVEGNGSTILFKPDPLIISKNHQRERATWLNNCDTNEPDTGQKYHG 308
 Db 240 PMFSGG-----TCNPOFVVQOLKVKIYSSNSGPTRR-----EDKF-- 274
 QY 309 FVSKRAYCFMVPEDAPVVEGDVRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 Db 275 -----MYFEFQPLPVC--GDIKVEFFHKQKMLKK---DKMFHFVWNTTFFIPGPEETS 323
 QY 359 -----ACDGLNG-GHFEYVDKTOPYIGDDTSIGRKNGMRRNETPMRKIDPETGNEFE 410
 Db 324 EKVENGLCDQBIIDSICSTERADNDKEYL-----VLTLTKNLDLKDANKKANKRYF 373
 QY 411 SP 412
 Db 374 SP 375

RESULT 3

US-08-906-156A-12
 ; Sequence 12, Application US/08906156A
 ; Patent No. 6287854
 ; GENERAL INFORMATION:
 ; APPLICANT: SPURR, NIGEL K
 ; APPLICANT: GRAY, IAN C
 ; APPLICANT: STEWART, LORNA M
 ; TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P. C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/906,156A
 ; FILING DATE: 05-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/042,655
 ; FILING DATE: 02-APR-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/033,147
 ; FILING DATE: 13-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/005,840
 ; FILING DATE: 23-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/96GB/02588
 ; FILING DATE: 22-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 1090-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 565 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

Db	121	SATAKRAISILQKKPRHQQLP	SLSSPFFSHRLPDMT	AIKEIYSRKNRRYQEDG	FDD	180	
Qy	69	CAYITDRIIAIGYATG	IEANFRSNKVQTOQ	FLTRHGHGKGNVKFN	LRGGYYVDADN	PDG 128	
Db	181	LTYYIPWIIANGFAER	LEGYVRNDDV	DFLDSKH-KNHVYK	YIYNLCAERHYD	AKFNC 239	
Qy	129	NVICFDMTDHHP	PSLEMAPREKAE	WLEADDDHVI	AVHCKAGKGRGT	GMICALLIYN 188	
Db	240	RVAGYPPEDHN	PPQLELIKPF	CEDDLQWL	SEDDNHVAIHC	KAGKGRGTGMICAYLLHRG 299	
Qy	189	FYPSPROILDYYS	IIRTKNNKGV	TIPSORRYIYY	YHKLREREL	NLPRLMQIGVYVERP 248	
Db	300	KFLKAQEA	LDFYGEV	RTDEKGV	TIPSORRYVY	YLLKNHLDYRPVALLPHKMMFETI 359	
Qy	249	PKTWGGSG	KIKVEVNGS	TILFPD	PLJISKSNIQR	ERATWLNCCDTPNEFDTG	BQOKYHG 308
Db	360	PMFSGG	-----TCNPFQ	VVQVLK	VKTIYSSNG	PTR-----EDKF-- 394	
Qy	309	FVSKRAYCEM	VPEDAPV	FVEGD	VRIDI--REIGFL	KFSDGKIGHWENTMF----- 358	
Db	395	-----MYFEP	QPLPVC--GDI	KVEFPHK	QNMKLK--DKMFH	FWNTFPDPEETS 443	
Qy	359	-----ACD	GGLNG-GHF	EYVDKTQ	PYIGD	DTISGRKNGWRNRNTPMKIDP	TGNEPE 410
Db	444	EKVENGSL	CQDEIS	CSIERAD	NDKYL-----VL	TKNDLKD	KANKRNYF 493
Qy	411	SP	412				
Db	494	SP	495				

RESULT 5
US-09-140-749-8
; Sequence 8, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavvighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3

```

? APPLICANT: Jasser, Samad
? APPLICANT: Yung, Alfred W.K.
? APPLICANT: Tavtigian, Sean V.
? TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
? FILE REFERENCE: 2318-205
? CURRENT APPLICATION NUMBER: US/09/140,749
? CURRENT FILING DATE: 1998-08-26
? EARLIER APPLICATION NUMBER: U.S. 08/791,115
? EARLIER FILING DATE: 1997-01-30
? EARLIER APPLICATION NUMBER: U.S. 60/057,750
? EARLIER FILING DATE: 1997-08-26
? EARLIER APPLICATION NUMBER: U.S. 60/083,563
? EARLIER FILING DATE: 1998-04-30
? NUMBER OF SEQ ID NOS: 64
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 8
? LENGTH: 597
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-140-749-8

```

Qy 69 CAVITDRIIAIGYPATGIEANFRNSKVQTQQFLTRHGKGNVKVFNLRGGYYVDADNFDG 128
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 219 LTVIYPNIIAMGPFAERLEGVRNNIDVVRFDSKH-KNHVKIYNLCAERHYDTAKENC 277

Qy 129 NVICFDMTDHHPPSLEIMAFPCREAKEWLEADDKHVIIAVHCCKAGKGRTGVNICALLIYIN 188

Db 278 RVAQPFEDHNPQLEIKPFCEDDLQWLSDDNHVAIHCAGKRGTVGWCAYLLHRG 337
QY 189 FYPSPRQLDYYSIIRTKNNKGVITPSQRRYIYYHKLREELNYLPLRMQLIGVYVERP 248
Db 338 KFLKAQEAALDFYGEVTRDKGVTIPSORRYVYVSYLLKNHLDYRVPVALLFKMMPETI 397
QY 249 PKTWGGGSKIKEVGVNGSTILFKPDPDLIIKSNHOREATWLNCDTNEFTDGEQKYHG 308
Db 398 PMFSGG-----TCNPQVWCQLKVKIYSSNSGPTRR-----EDKP-- 432
QY 309 FVSKRAYCFMVPEDAPVFEVGDVRDI--REIGFLKPFSDGKIGHVWENTMF-- 358
Db 433 -----MYFEPQPLPVC--GDIKVEFFHKQNMKK--DKMFHFWNTTFIPGPEETS 481
QY 359 -----ACDGLGNG--GHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFE 410
Db 482 EKVENGLCDQEIIDSICSIERADNDKEYL-----VLTLTCKNDLCKANKDKANRYF 531
QY 411 SP 412
Db 532 SP 533

RESULT 6

US-08-791-115B-6
; Sequence 6, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-6
Query Match 9.8%; Score 507; DB 3; Length 645;
Best Local Similarity 30.6%; Pred. No. 3.8e-34;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

Db 207 SATAKSRAISILQKKPRHQQLLPSLSFFFSHRLPDMTALIKEIVSRNKRRYQEDGFDLD 266
QY 69 CAYTDRILAIAGYPATGIEANFRNSKVOTQOFLTRRHGKGNVKNVFNLRGGYVYADNFDG 128
Db 267 LTYIYVNPNIAMGFFPAERLEGVYRNIDDDVRFLLSKH-KNHYKIYNLCARHYDTAKFNC 325
QY 129 NVICFDMTDHPPSPSLEMAPECREAKWLEADDKHVIAVHCAGKAGRGVIMICALLIYIN 188
Db 326 RVAQPFEDHNPQLEIKPFCEDDLQWLSDDNHVAIHCAGKRGTVGWCAYLLHRG 385
QY 189 FYPSPRQLDYYSIIRTKNNKGVITPSQRRYIYYHKLREELNYLPLRMQLIGVYVERP 248
Db 386 KFLKAQEAALDFYGEVTRDKGVTIPSORRYVYVSYLLKNHLDYRVPVALLFKMMPETI 445
QY 249 PKTWGGGSKIKEVGVNGSTILFKPDPDLIIKSNHOREATWLNCDTNEFTDGEQKYHG 308
Db 446 PMFSGG-----TCNPQVWCQLKVKIYSSNSGPTRR-----EDKP-- 480
QY 309 FVSKRAYCFMVPEDAPVFEVGDVRDI--REIGFLKPFSDGKIGHVWENTMF-- 358
Db 481 -----MYFEPQPLPVC--GDIKVEFFHKQNMKK--DKMFHFWNTTFIPGPEETS 529
QY 359 -----ACDGLGNG--GHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFE 410
Db 530 EKVENGLCDQEIIDSICSIERADNDKEYL-----VLTLTCKNDLCKANKDKANRYF 579
QY 411 SP 412
Db 580 SP 581

RESULT 7

US-08-791-115B-5
; Sequence 5, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 742 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-5

Query Match 9.8%; Score 507; DB 3; Length 742;
Best Local Similarity 30.6%; Pred. No. 4.8e-34;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTESMAED-LOENPNQPGEPVSEPHNSIVERIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 304 SATAKSRAISILOKPRHQQLPSLSFFSHRLPDMTAIKEIIVSRNKRRYQEDGFDLD 363

QY 69 CAYITDRIIAGYPATGIEANFRNSKVQOQFLTRRHGKGVNLFNLGRGGYVYDADNFDG 128
DB 364 LTYIYPNIIAMGFPARLEGVYRNIDDVVRLDSKH-KHYKIYNLCARHYDTAKENC 422

QY 129 NVICFDMTHHPSPLELMAPPCEAKEMLEADKHVIAVHCAGKGRGTGWMICALLIYN 188
DB 423 RVAQYPPFEDHNPQLELIKPFCEDLQWLSSEDDNVAATHCAGKGRGTGWMICAYLLHRG 482

QY 189 FYPSPQILDYYSIIRTKNNKGVITIPSORRYIYYHKLREERLNYLPLRMQLIGVYVERP 248
DB 483 KFLKAQALDFGEVTRDKKGVITIPSORRYIYYHKLREERLNYLPLRMQLIGVYVERP 542

QY 249 PXTWGGGKIKVEVNGSTILFKPDPLIISKSNHORERATWLNCCDTPNEFDTGQKYHG 308
DB 543 PMFSGG-----TCNPQFVVCQKVIYSSNSGPTRR-----EDKF-- 577

QY 309 FVSKRAYCPMVPEDAPVFEVDVRI--REIGFLKFSDGKIGHVWNTMF----- 358
DB 578 -----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK--DKMFHFWNTTFFIPGPEETS 626

QY 359 -----ACDGLGNG-GHPEYVDKTPYIGDDTSIGRKNMERTPMRKIDPETGNEFFE 410
DB 627 EKVENSLCQDEIDSICSIERADNDKEYL-----VLTITKNDLKDANKOKANRYF 676

QY 411 SP 412
DB 677 SP 678

RESULT 8
US-08-791-115B-27
; Sequence 27, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031

Query Match 9.5%; Score 490.5; DB 4; Length 394;
Best Local Similarity 31.3%; Pred. No. 4.4e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRFVAVSNRTEYQNIIDLCAVITDRIIAGYPATGIEANFRNSKVQOQFLTRRHGK 107
DB 4 IIKEIVSRNKRRYQEDGFDLDLTYIPNIIAMGFPARLEGVYRNIDDVVRLDSKH-K 62

QY 108 GNVKVENLRGGYVYDADNFDGVCVTCFMDTHHPSPLELMAPPCEAKEMLEADKHVIAV 167
DB 63 NHYKIYNLCARHYDTAKFNCVQAQYFEDHNPQLELIKPFCEDLQWLSSEDDNVAAI 122

QY 168 HCKAGKGRGTGWMICALLIYNFYPSPQILDYYSIIRTKNNKGVITIPSORRYIYYHKL 227
DB 123 HCKAGKGRGTGWMICAYLLHRGKFLKAQALDFGEVTRDKKGVITIPSORRYIYYHKL 182

QY 228 BRENLPLRMQLIGVYVERPPTWGGGSKIKEVNGSTILFKPDPLIISKSNHORERA 287
DB 183 KNHLDYRVPALLFHKMPETIEMFSGG-----TCNPQFVVCQKVIYSSNSGPTRR-- 234

QY 288 TWLNCCDTPNEFDTGQKYHGVSKRAYCFMVPEDAPVFEVDVRI--REIGFLKFS 345
DB 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLGNG-GHPEYVDKTPYIGDDTSIGRKN 389
DB 268 -DKMFHFWNTTFFIPGPEETSEKVENSLCQDEIDSICSIERADNDKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
DB 317 VLTITKNDLKDANKOKANRYFSP 339

RESULT 9
US-09-140-749-17
; Sequence 17, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-17

Query Match 9.5%; Score 490.5; DB 4; Length 394;
Best Local Similarity 31.3%; Pred. No. 4.4e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

US-08-791-115B-23

Query Match 9.5%; Score 490.5; DB 3; Length 403;
 Best Local Similarity 31.3%; Pred. No. 4.6e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAGYPAATGIEANFRNSKVQTOQFLTRRHGK 107
 DB 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62

QY 108 G N V K F N L R G G Y Y D A N D F G N V I C F D M T D H P P S L E M A P F C R E A K E W L E A D D K H V I A V 167
 DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S Q R R Y V I Y Y H K L R 227
 DB 123 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S Q R R Y V I Y Y H K L R 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N S T I L F K P D P L I I S K S N H Q R E R A 287
 DB 183 K N H L D Y R P V A L L F H K M P E T I P M F S G G - - - - - T C N P Q V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N N C D T N E F D T G E Q K Y H G F V S K R A Y C F W P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
 DB 235 - - - - - E D K F - - - - - M Y F E P P Q L P V C - - G D I K V E F F H K N K M L K - - 267

QY 346 D G K I G H V W F N T M F - - - - - A C D G L N G - G H F E Y V D K T Q P Y I G D T S I G R K N 389
 DB 268 - D K M F H F W N T F I P G P E E T S E K V E N S L C D Q E I D S I E R A D N D K E Y L - - - - - 316

QY 390 G M R N E T P M R K I D P E T G N E F E S P 412
 DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 12

US-08-791-115B-25
 ; Sequence 25, Application US/08791115B
 ; Patent No. 6262242
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, W.K. Alfred
 ; APPLICANT: Tavtighian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
 ; STREET: 555 Thirteenth Street, N.W., Suite 701-E
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 22204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,115B
 ; FILING DATE: 30-JAN-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Innen, Jeffrey L.
 ; REGISTRATION NUMBER: 38,957
 ; REFERENCE/DOCKET NUMBER: 2318-134.A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-683-6040
 ; TELEFAX: 202-683-7031
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 403 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-791-115B-25

Query Match 9.5%; Score 490.5; DB 3; Length 403;
 Best Local Similarity 31.3%; Pred. No. 4.6e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAGYPAATGIEANFRNSKVQTOQFLTRRHGK 107
 DB 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62

QY 108 G N V K F N L R G G Y Y D A N D F G N V I C F D M T D H P P S L E M A P F C R E A K E W L E A D D K H V I A V 167
 DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S Q R R Y V I Y Y H K L R 227
 DB 123 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S Q R R Y V I Y Y H K L R 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N S T I L F K P D P L I I S K S N H Q R E R A 287
 DB 183 K N H L D Y R P V A L L F H K M P E T I P M F S G G - - - - - T C N P Q V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N N C D T N E F D T G E Q K Y H G F V S K R A Y C F W P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
 DB 235 - - - - - E D K F - - - - - M Y F E P P Q L P V C - - G D I K V E F F H K N K M L K - - 267

QY 346 D G K I G H V W F N T M F - - - - - A C D G L N G - G H F E Y V D K T Q P Y I G D T S I G R K N 389
 DB 268 - D K M F H F W N T F I P G P E E T S E K V E N S L C D Q E I D S I E R A D N D K E Y L - - - - - 316

QY 390 G M R N E T P M R K I D P E T G N E F E S P 412
 DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 13

US-09-140-749-2
 ; Sequence 2, Application US/09140749
 ; Patent No. 6482795
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, Alfred W.K.
 ; APPLICANT: Tavtighian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; FILE REFERENCE: 2318-205
 ; CURRENT APPLICATION NUMBER: US/09/140,749
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: U.S. 08/791,115
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER APPLICATION NUMBER: U.S. 60/057,750
 ; EARLIER FILING DATE: 1997-08-26
 ; EARLIER APPLICATION NUMBER: U.S. 60/083,563
 ; EARLIER FILING DATE: 1998-04-30
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-140-749-2

Query Match 9.5%; Score 490.5; DB 4; Length 403;
 Best Local Similarity 31.3%; Pred. No. 4.6e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAGYPAATGIEANFRNSKVQTOQFLTRRHGK 107
 DB 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62

```

QY 108 GNVKFNLRGGYYADNFDGNVICFDMTDHPPSLELMAPCRKAEKWLADDDKHVIAV 167
Db 63 NHYKIYNLCAERHYDTAKFNCRAVQYPPFEDHPPQLELIKPFCDLQWLSDDNHVAAI 122

QY 168 HCKAGKGRGVMICALLIYINFPSPROILDYYSIIRTKNNKGVTPISORRYIYYHKL 227
Db 123 HCKAGKGRGVMICALLHRGFLKAQALDFYGEVRTDKGVTPISORRYIYYSYLL 182

QY 228 ERELNYLPLRMQLIGYVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERA 287
Db 183 KNLHDYRVPVALLFHKKMFETIPMFSGG-----TCNPQVVCQLKVKIYSSNGPTRR- 234

QY 288 TWLNCDTPNEFDTEQKYHGFVSKRAYCFMVPEADPVFVGVDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLKDANKOKANRYFSP 339

RESULT 14
US-09-140-749-10
; Sequence 10, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-10

Query Match 9.5%; Score 490.5; DB 4; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRTAVSSNRCRTEYQNIDLCAVITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
Db 4 IIEIVSRNKRKYQEDGFDLDTIYIPNIANGFPAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNFDGNVICFDMTDHPPSLELMAPCRKAEKWLADDDKHVIAV 167
Db 63 NHYKIYNLCAERHYDTAKFNCRAVQYPPFEDHPPQLELIKPFCDLQWLSDDNHVAAI 122

QY 168 HCKAGKGRGVMICALLIYINFPSPROILDYYSIIRTKNNKGVTPISORRYIYYHKL 227
Db 123 HCKAGKGRGVMICALLHRGFLKAQALDFYGEVRTDKGVTPISORRYIYYSYLL 182

QY 228 ERELNYLPLRMQLIGYVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERA 287
Db 183 KNLHDYRVPVALLFHKKMFETIPMFSGG-----TCNPQVVCQLKVKIYSSNGPTRR- 234

QY 288 TWLNCDTPNEFDTEQKYHGFVSKRAYCFMVPEADPVFVGVDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLKDANKOKANRYFSP 339

```

```

QY 288 TWLNCDTPNEFDTEQKYHGFVSKRAYCFMVPEADPVFVGVDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLKDANKOKANRYFSP 339

RESULT 15
US-09-140-749-49
; Sequence 49, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-49

Query Match 9.5%; Score 490.5; DB 4; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRTAVSSNRCRTEYQNIDLCAVITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
Db 4 IIEIVSRNKRKYQEDGFDLDTIYIPNIANGFPAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNFDGNVICFDMTDHPPSLELMAPCRKAEKWLADDDKHVIAV 167
Db 63 NHYKIYNLCAERHYDTAKFNCRAVQYPPFEDHPPQLELIKPFCDLQWLSDDNHVAAI 122

QY 168 HCKAGKGRGVMICALLIYINFPSPROILDYYSIIRTKNNKGVTPISORRYIYYHKL 227
Db 123 HCKAGKGRGVMICALLHRGFLKAQALDFYGEVRTDKGVTPISORRYIYYSYLL 182

QY 228 ERELNYLPLRMQLIGYVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERA 287
Db 183 KNLHDYRVPVALLFHKKMFETIPMFSGG-----TCNPQVVCQLKVKIYSSNGPTRR- 234

QY 288 TWLNCDTPNEFDTEQKYHGFVSKRAYCFMVPEADPVFVGVDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLKDANKOKANRYFSP 339

```

Search completed: December 10, 2003, 20:35:43
Job time : 24.8315 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:34:18 ; Search time 42.9968 Seconds
(without alignments)
4170.856 Million cell updates/sec

Title: US-09-205-658A-310
Perfect score: 5168
Sequence: 1 MVTTPDPVSTSTRSMARDL.....IAHPSNSFSDSNFDQAIYL 962

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5168	100.0	962	9 US-09-205-658-310	Sequence 310, Appl
2	5168	100.0	962	12 US-09-963-693-310	Sequence 310, Appl
3	1330	25.7	248	9 US-09-205-658-308	Sequence 308, Appl
4	1330	25.7	248	12 US-09-963-693-308	Sequence 308, Appl
5	508.5	9.8	430	12 US-10-299-003-18	Sequence 18, Appl
6	507	9.8	559	12 US-10-299-003-15	Sequence 15, Appl
7	507	9.8	597	12 US-10-299-003-8	Sequence 8, Appl
8	490.5	9.5	394	12 US-10-299-003-17	Sequence 17, Appl
9	490.5	9.5	403	10 US-09-870-379-2	Sequence 2, Appl
10	490.5	9.5	403	12 US-10-299-003-2	Sequence 2, Appl
11	490.5	9.5	403	12 US-10-299-003-10	Sequence 10, Appl
12	490.5	9.5	403	12 US-10-299-003-49	Sequence 49, Appl
13	490.5	9.5	403	12 US-10-299-003-55	Sequence 55, Appl
14	490.5	9.5	403	12 US-10-299-003-57	Sequence 57, Appl
15	490.5	9.5	403	15 US-10-059-585-50	Sequence 50, Appl

16	465	9.0	249	9 US-09-205-658-309	Sequence 309, Appl
17	465	9.0	249	12 US-09-963-693-309	Sequence 309, Appl
18	368	7.1	445	12 US-10-120-801-99	Sequence 99, Appl
19	342	6.6	645	12 US-10-120-801-101	Sequence 101, Appl
20	342	6.6	664	12 US-10-120-801-100	Sequence 100, Appl
21	333.5	6.5	551	12 US-10-120-801-97	Sequence 97, Appl
22	333.5	6.5	551	12 US-10-120-801-98	Sequence 98, Appl
23	333.5	6.5	551	15 US-10-059-585-50	Sequence 57, Appl
24	321	6.2	477	12 US-10-120-801-30	Sequence 30, Appl
25	236	4.6	85	9 US-09-864-761-37705	Sequence 37705, A
26	236	4.6	86	12 US-10-029-386-30662	Sequence 30662, A
27	213	4.1	1386	12 US-10-327-414-2	Sequence 2, Appl
28	210	4.1	382	12 US-10-327-414-4	Sequence 4, Appl
29	206	4.0	1300	12 US-10-102-549-2	Sequence 2, Appl
30	206	4.0	1311	12 US-10-354-358-68	Sequence 68, Appl
31	153.5	3.0	862	12 US-10-339-782-492	Sequence 492, Appl
32	153.5	3.0	910	15 US-10-177-293-449	Sequence 449, Appl
33	150	2.9	1369	9 US-09-729-674-42	Sequence 42, Appl
34	136	2.6	991	9 US-09-815-242-5803	Sequence 5803, Ap
35	136	2.6	1053	15 US-10-217-700-6	Sequence 6, Appl
36	135.5	2.6	543	12 US-10-032-585-7649	Sequence 7649, Ap
37	135	2.6	1884	10 US-09-785-770A-17	Sequence 17, Appl
38	135	2.6	1907	10 US-09-785-770A-16	Sequence 16, Appl
39	133.5	2.6	1054	9 US-09-376-045-4	Sequence 4, Appl
40	130.5	2.5	980	9 US-09-888-615-65	Sequence 65, Appl
41	130.5	2.5	1054	15 US-10-217-700-3	Sequence 3, Appl
42	126.5	2.4	1616	11 US-09-820-843A-16	Sequence 16, Appl
43	126.5	2.4	1863	10 US-09-734-672-4	Sequence 4, Appl
44	126.5	2.4	1863	11 US-09-982-828-6	Sequence 6, Appl
45	126	2.4	745	12 US-10-032-585-7860	Sequence 7860, Ap

ALIGNMENTS

RESULT 1

US-09-205-658-310
; Sequence 310, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 962
; TYPE: PPT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-310

Query Match 100.0%; Score 5168; DB 9; Length 962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVTTPDPVSTSTRSMARDLQENPNRQGPPEPVHNSIVERIRHIFRTAVSNRCRT	60
Db	1	MVTTPDPVSTSTRSMARDLQENPNRQGPPEPVHNSIVERIRHIFRTAVSNRCRT	60
Qy	61	EYQNDLDCAVITDRIITAIIGYPATGIEANFNSKVQTOOFLTRRHCKGNKVNLRGGYY	120
Db	61	EYQNDLDCAVITDRIITAIIGYPATGIEANFNSKVQTOOFLTRRHCKGNKVNLRGGYY	120

```

QY 121 YDADNFDGNVICFDMTHDHPSPLELMAPECREAKEWLEADDKHVI AVHCKAGKRTGVM 180
DB 121 YDADNFDGNVICFDMTHDHPSPLELMAPECREAKEWLEADDKHVI AVHCKAGKRTGVM 180
QY 181 CALLIYINFPSPQRIIDYYSIIRTKNNKGVITPSQRRYIYYHKLRERELNYLPLRMQL 240
DB 181 CALLIYINFPSPQRIIDYYSIIRTKNNKGVITPSQRRYIYYHKLRERELNYLPLRMQL 240
QY 241 IGVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTPNEFD 300
DB 241 IGVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTPNEFD 300
QY 301 TGEQKHGFSKRAYCFMVPEDAPVFEVDVIRIDIREIGFLKFKSGDKIGHVWNTMFAC 360
DB 301 TGEQKHGFSKRAYCFMVPEDAPVFEVDVIRIDIREIGFLKFKSGDKIGHVWNTMFAC 360
QY 361 DGLGNGGHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
DB 361 DGLGNGGHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
QY 421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDRKLPMDGKSYTESGK 480
DB 421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDRKLPMDGKSYTESGK 480
QY 481 SGDIRGVGGPFEIPIYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCVDTROSKME 540
DB 481 SGDIRGVGGPFEIPIYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCVDTROSKME 540
QY 541 KSEVFGNLAHFNESTRRLQALQTMNPKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKYNGA 600
DB 541 KSEVFGNLAHFNESTRRLQALQTMNPKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKYNGA 600
QY 601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKRFYCPPLIKKHFIYPADTDDVD 660
DB 601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKRFYCPPLIKKHFIYPADTDDVD 660
QY 661 ENGQPFPHSPHYIKEQEKIDAEKAGIENTGPTSGSSAPGTIKKTEASQSKVKPAT 720
DB 661 ENGQPFPHSPHYIKEQEKIDAEKAGIENTGPTSGSSAPGTIKKTEASQSKVKPAT 720
QY 721 EDELPPARLPDNRVRRFPVVGVDNFENPEESCEHKTVESIAGFEPLEHLFHESYHPNTAGN 780
DB 721 EDELPPARLPDNRVRRFPVVGVDNFENPEESCEHKTVESIAGFEPLEHLFHESYHPNTAGN 780
QY 781 MLRQDYHTDSEVKIAEQEAKAFVDQLLNGQGVLPQBFMKQFVPSDNSFADYVTGQAEVFK 840
DB 781 MLRQDYHTDSEVKIAEQEAKAFVDQLLNGQGVLPQBFMKQFVPSDNSFADYVTGQAEVFK 840
QY 841 AQIALLEQSEDFORVOANAEVDLEHTLGEAFERGHVVEESNGSKNPKALKTREQMVK 900
DB 841 AQIALLEQSEDFORVOANAEVDLEHTLGEAFERGHVVEESNGSKNPKALKTREQMVK 900
QY 901 ETGKDTQKTRNVLHLLEANHRVQIERRETCTPELHPEDKIPRIAHFSENSFSDSNFDQAI 960
DB 901 ETGKDTQKTRNVLHLLEANHRVQIERRETCTPELHPEDKIPRIAHFSENSFSDSNFDQAI 960
QY 961 YL 962
DB 961 YL 962

```

RESULT 2

```

US-09-963-693-310
; Sequence 310, Application US/09963693
; Publication No. US200301813641
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25

```

```

; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-310

Query Match 100.0%; Score 5168; DB 12; Length 962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTPTTVPSTSTSMARDLOENPNRQPGSEPRVSEPHVNSIVIRIRHIFRTAVSSNRCT 60
DB 1 MVTPTTVPSTSTSMARDLOENPNRQPGSEPRVSEPHVNSIVIRIRHIFRTAVSSNRCT 60
QY 61 EYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOOFLTRRHGKGNVKNLRCGGY 120
DB 61 EYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOOFLTRRHGKGNVKNLRCGGY 120
QY 121 YDADNFDGNVICFDMTHDHPSPLELMAPECREAKEWLEADDKHVI AVHCKAGKRTGVM 180
DB 121 YDADNFDGNVICFDMTHDHPSPLELMAPECREAKEWLEADDKHVI AVHCKAGKRTGVM 180
QY 181 CALLIYINFPSPQRIIDYYSIIRTKNNKGVITPSQRRYIYYHKLRERELNYLPLRMQL 240
DB 181 CALLIYINFPSPQRIIDYYSIIRTKNNKGVITPSQRRYIYYHKLRERELNYLPLRMQL 240
QY 241 IGVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTPNEFD 300
DB 241 IGVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTPNEFD 300
QY 301 TGEQKHGFSKRAYCFMVPEDAPVFEVDVIRIDIREIGFLKFKSGDKIGHVWNTMFAC 360
DB 301 TGEQKHGFSKRAYCFMVPEDAPVFEVDVIRIDIREIGFLKFKSGDKIGHVWNTMFAC 360
QY 361 DGLGNGGHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
DB 361 DGLGNGGHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
QY 421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDRKLPMDGKSYTESGK 480
DB 421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDRKLPMDGKSYTESGK 480
QY 481 SGDIRGVGGPFEIPIYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCVDTROSKME 540
DB 481 SGDIRGVGGPFEIPIYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCVDTROSKME 540
QY 541 KSEVFGNLAHFNESTRRLQALQTMNPKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKYNGA 600
DB 541 KSEVFGNLAHFNESTRRLQALQTMNPKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKYNGA 600
QY 601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKRFYCPPLIKKHFIYPADTDDVD 660
DB 601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKRFYCPPLIKKHFIYPADTDDVD 660
QY 661 ENGQPFPHSPHYIKEQEKIDAEKAGIENTGPTSGSSAPGTIKKTEASQSKVKPAT 720
DB 661 ENGQPFPHSPHYIKEQEKIDAEKAGIENTGPTSGSSAPGTIKKTEASQSKVKPAT 720
QY 721 EDELPPARLPDNRVRRFPVVGVDNFENPEESCEHKTVESIAGFEPLEHLFHESYHPNTAGN 780
DB 721 EDELPPARLPDNRVRRFPVVGVDNFENPEESCEHKTVESIAGFEPLEHLFHESYHPNTAGN 780
QY 781 MLRQDYHTDSEVKIAEQEAKAFVDQLLNGQGVLPQBFMKQFVPSDNSFADYVTGQAEVFK 840

```

Db 781 MLRQYHDTSEVKIAEQEAKAFVDQLLNGGVQLQFMKQFVPSNSFADYVTGQAEVFK 840
Qy 841 AQIALLESQEDFORVQANAEVDLSEHTLGEAFERFCHVVEESGSKNPKALKKTREQMVK 900
Db 841 AQIALLESQEDFORVQANAEVDLSEHTLGEAFERFCHVVEESGSKNPKALKKTREQMVK 900
Qy 901 ETGKDTOKTRNHVLHLEAHNRHVOIERRETCTELHPEDKIPRIAHFSENSFSDSNFDOAI 960
Db 901 ETGKDTOKTRNHVLHLEAHNRHVOIERRETCTELHPEDKIPRIAHFSENSFSDSNFDOAI 960
Qy 961 YL 962
Db 961 YL 962

RESULT 3

US-09-205-658-308
; Sequence 308, Application US/09205658
; Patent No. US20010029617A1

GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; IMPAIRED GLUCOSE TOLERANCE CONDITIONS

; FILE REFERENCE: 00786/351004

; CURRENT APPLICATION NUMBER: US/09/205,658

; PRIOR FILING DATE: 1998-12-03

; EARLIER APPLICATION NUMBER: 08/857,076

; EARLIER FILING DATE: 1997-05-15

; EARLIER APPLICATION NUMBER: 08/888,534

; EARLIER FILING DATE: 1997-07-07

; EARLIER APPLICATION NUMBER: US98/10080

; EARLIER FILING DATE: 1998-05-15

; NUMBER OF SEQ ID NOS: 328

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 308

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-205-658-308

Query Match 25.7%; Score 1330; DB 9; Length 248;

Best Local Similarity 99.2%; Pred. No. 2.3e-98;

Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 48 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 1 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 60
Qy 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 167
Db 61 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 120
Qy 168 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVTPSORRYIYYHKL 227
Db 121 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVTPSORRYIYYHKL 180
Qy 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPLIISKSNHQRERA 287
Db 181 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPLIISKSNHQRERA 240
Qy 288 TWLNACDT 295
Db 241 TWLNACDT 248

RESULT 4

US-09-963-693-308

; Sequence 308, Application US/09963693

; Publication No. US20030181364A1

GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary

; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; IMPAIRED GLUCOSE TOLERANCE CONDITIONS

; FILE REFERENCE: 00786/351004

; CURRENT APPLICATION NUMBER: US/09/963,693

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/205,658

; PRIOR FILING DATE: 1998-12-03

; PRIOR APPLICATION NUMBER: 08/857,076

; PRIOR FILING DATE: 1997-05-15

; PRIOR APPLICATION NUMBER: 08/888,534

; PRIOR FILING DATE: 1997-07-07

; PRIOR APPLICATION NUMBER: US98/10080

; PRIOR FILING DATE: 1998-05-15

; NUMBER OF SEQ ID NOS: 328

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 308

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-963-693-308

Query Match 25.7%; Score 1330; DB 12; Length 248;

Best Local Similarity 99.2%; Pred. No. 2.3e-98;

Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 48 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 1 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 60
Qy 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 167
Db 61 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 120
Qy 168 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVTPSORRYIYYHKL 227
Db 121 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVTPSORRYIYYHKL 180
Qy 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPLIISKSNHQRERA 287
Db 181 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPLIISKSNHQRERA 240
Qy 288 TWLNACDT 295
Db 241 TWLNACDT 248

RESULT 5

US-10-299-003-18

; Sequence 18, Application US/10299003

; Publication No. US20030139324A1

GENERAL INFORMATION:

; APPLICANT: Steck, Peter

; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jasser, Samar

; APPLICANT: Yung, Alfred W.K.

; APPLICANT: Tavtigan, Sean V.

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3

; FILE REFERENCE: 2318-385

; CURRENT APPLICATION NUMBER: US/10/299,003

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: U.S. 09/140,749

; PRIOR FILING DATE: 1998-08-26

; PRIOR APPLICATION NUMBER: U.S. 08/791,115

; PRIOR FILING DATE: 1997-01-30

; PRIOR APPLICATION NUMBER: U.S. 60/057,750

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: U.S. 60/083,563

; PRIOR FILING DATE: 1998-04-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 430

```

; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-18

```

```

Query Match          9.8%; Score 508.5; DB 12; Length 430;
Best Local Similarity 30.3%; Pred. No. 3.8e-32;
Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;

```

```

QY 9 PSTSTRMARDLOENPNRQPGPRVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 1 PPAARFGAACSLRRPRRPPPLPSLSSFLSSHRLPDMTAAIKIIVSRNKRRYQEDGFDL 60
QY 69 CAYITDRIIAGVPATGIEANFRNSKVQOQLTRRHGKGNVKNLRCGGVYDADNFDG 128
DB 61 LTYIYPNIIAMGFFPAERLEGVTRNNIDVVRFLDSKH-KNHKYIYNLCAERHYDTAKFNC 119
QY 129 NVICFDMTDHPPSLEMAPFCREAKEWLEADDKHVIAVHCKAGKGRGTGMICALLIYN 188
DB 120 RVAQYFFEDHNPQLELIKPFCELDQWLSDDNHVAIHCKAGKGRGTGMICAYLLHRG 179
QY 189 FYPSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
DB 180 KFLKAQEAALDFYGEVTRDKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
QY 249 PKTWGGGSKIKEVNGSGTILFKPDPLIISKSNHQRERATWLNCDTNEPFTGQKYHG 308
DB 240 PMFSGG-----TCNPQFVVCQKVKIYSSNSGPTRR-----EDKF-- 274
QY 309 FVSKRAYCFMVPEDAPVFEVDGVRIDI--REIGFLKFFSDGKIGHVWFTMTF----- 358
DB 275 -----MYFEFPQPLPVC--GDIKVEFFHKQNKMLKK---DKMFHFVWNTFFIPGPEETS 323
QY 359 -----ACDGLGNG-GHFEYVDKTPQYIGDDTSIGRKNMGRNETPMRKIDPETGNEFE 410
DB 324 EKVENGLCDQEIIDSICSIERADNDKEYL-----VLTITKNDLCKANKKANYF 373
QY 411 SP 412
DB 374 SP 375

```

```

RESULT 6
US-10-299-003-15
; Sequence 15, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-15
Query Match          9.8%; Score 507; DB 12; Length 559;
Best Local Similarity 30.6%; Pred. No. 7.6e-32;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

```

```

QY 10 STSTRMARDLOENPNRQPGPRVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 159 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRRYQEDGFDL 218

```



```
QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKANDKANYFSP 339

RESULT 10
US-10-299-003-2
; Sequence 2, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-2

Query Match 9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRATVSSNRCRTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVOTQOFLTRRHGK 107
Db 4 LIKEIVSRNKRKYQEDGFDLDLTIIYPNIIANGPFAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNFDGNVICFDMTDHHPSPLELMAPFCRAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCARHYDTAKFNCRAQYPPEDHNPQLELIKPFCELDQWLSDDNHVAI 122

QY 168 HCKAGKRGTMICALLIYINFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227
Db 123 HCKAGKRGTMICAYLLHRGKFLKAQALDYGEVTRDKKGVTIPSORRYIYYSYLL 182

QY 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKI KVEVNGSTILFKPDPPLIISKSNHQRERA 287
Db 183 KNLHLYRPVALLFKHMPETIPMFSGG-----TCNPQFVVQQLKVKIYSSNSGPTRR- 234

QY 288 TWLNCDTNEFDTEGQKHGFSKRAYCFMVPEDAPVFVEGDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCDQEIDSICSIERANDNKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKANDKANYFSP 339

RESULT 11
US-10-299-003-10
; Sequence 10, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-10

Query Match 9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRATVSSNRCRTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVOTQOFLTRRHGK 107
Db 4 LIKEIVSRNKRKYQEDGFDLDLTIIYPNIIANGPFAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNFDGNVICFDMTDHHPSPLELMAPFCRAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCARHYDTAKFNCRAQYPPEDHNPQLELIKPFCELDQWLSDDNHVAI 122

QY 168 HCKAGKRGTMICALLIYINFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227
Db 123 HCKAGKRGTMICAYLLHRGKFLKAQALDYGEVTRDKKGVTIPSORRYIYYSYLL 182

QY 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKI KVEVNGSTILFKPDPPLIISKSNHQRERA 287
Db 183 KNLHLYRPVALLFKHMPETIPMFSGG-----TCNPQFVVQQLKVKIYSSNSGPTRR- 234

QY 288 TWLNCDTNEFDTEGQKHGFSKRAYCFMVPEDAPVFVEGDVRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCDQEIDSICSIERANDNKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKANDKANYFSP 339

RESULT 12
US-10-299-003-49
; Sequence 49, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
```

```

; LENGTH: 403
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-55

Query Match          9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

Qy  48 IFTAVSSNCRTEYQNIIDLDCAVITDRIITAIGYPATGIEANFRNSKVQTQOFLTRHGK 107
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  108 GNVKVFNLRGYYYYADNFDGNVICFDMTDHHPSPSELMAFPFCREAKEWLEADDKHVI 167
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  168 HCKAGKRTGVMICALLIYINFPSPQIILDYISITRTKNKGVTIIPSORRYIYYHKLR 227
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  123 HCKAGKRTGVMICAYLLHKGKFKAQEALDFYGEVTRDKGVTIIPSORRYIYYYSYLL 182
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  228 ERELNLPLRMQLIGVVVERPPKTTGGGSKIKEVGVNGSTILPKPDPPLIISKSNHQERA 287
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  183 KNHLDRVPVALLPHKMFPETIPFSGG-----TCNPQFVQOLKVKIYSSNSGPTRR- 234
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  288 TWLNCCDTPNEFDTGEOKYHGFVSKRAYCFMWPEDAPFVFGVDGRIDI--REIGFLKKFS 345
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  235 -----EDKF-----MYEFFPQPLPVC--GDIKVEFFHKQNMKMK-- 267
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  346 DGKIGHWFNTMP-----ACDGGING-GHFEYVDKTPYIGDDTSIGRKN 389
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  390 GMRNRTPMRKIDPETGNEPESP 412
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy  317 VLTLTKNDLKDANKDKANRYFSP 339
Db   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 14
US-10-299-003-57
; Sequence 57, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar

```

```

; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-299-003-57

Query Match          9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
48 IPTAVSSNRCREYONIDIDCAVITDRTIAIGVDPATGIRANPNSKVOTQOFTTPEHGK 107

```

Db 4 I I K E I V S R N K R R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H - K 62
QY 108 G N V K V N L R G G Y Y D A D N F D G N V I C F D M T D H H P P S L E L M A P C R E A K E W L E A D D K H V I A V 167
Db 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I 122
QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
Db 123 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 182
QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N S T I L F K P D P L I I S K S N H Q R E R A 287
Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V K I Y S N S G P T R R - 234
QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F V E G D V R I D I - - R E I G F L K K F S 345
Db 235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K Q N K M L K K - - 267
QY 346 D G K I G H W F N T M F - - - - - A C D G G L N G - G H F E Y V D K T Q P Y I G D T S I G R K N 389
Db 268 - D K M F H F W N T F F I P G P E T S E K V E N S L C D Q E I D S I E R A D N D K E Y L - - - - - 316
QY 390 G M R N E T P M R K I D P E T G N E F E S P 412
Db 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 15
US-10-059-585-50
; Sequence 50, Application US/10059585
; Publication No. US220030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayaashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-50

Query Match 9.5%; Score 490.5; DB 15; Length 403;

Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
QY 48 I P R T A V S N R O R T E Y Q N I D L D C A Y I T D R I I A I G Y P A T G I E A N F R N S K V Q T O Q F L T R R H G K 107
Db 4 I I K E I V S R N K R R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H - K 62
QY 108 G N V K V N L R G G Y Y D A D N F D G N V I C F D M T D H H P P S L E L M A P C R E A K E W L E A D D K H V I A V 167
Db 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I 122
QY 168 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
Db 123 H C K A G K G R T G V M I C A L L I Y I N F Y P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 182
QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N S T I L F K P D P L I I S K S N H Q R E R A 287
Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V K I Y S N S G P T R R - 234
QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F V E G D V R I D I - - R E I G F L K K F S 345
Db 235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K Q N K M L K K - - 267
QY 346 D G K I G H W F N T M F - - - - - A C D G G L N G - G H F E Y V D K T Q P Y I G D T S I G R K N 389
Db 268 - D K M F H F W N T F F I P G P E T S E K V E N S L C D Q E I D S I E R A D N D K E Y L - - - - - 316
QY 390 G M R N E T P M R K I D P E T G N E F E S P 412
Db 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

Search completed: December 10, 2003, 20:43:26
Job time : 43.8968 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:07 ; Search time 27.8035 Seconds
(without alignments)
3327.436 Million cell updates/sec

Title: US-09-205-658A-310
Perfect score: 5168
Sequence: 1 MVTPEPDPVSTSTRSMARDL.....IAHPSNSFSDSNFDQAIYL 962

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5168	100.0	962	T51924	daf-18 protein - C
2	5156.5	99.8	965	T32574	hypothetical prote
3	437	8.5	628	T45864	probable tyrosine
4	283	5.5	1792	A57075	tensin - chicken (
5	281	5.4	1744	A54970	tensin - chicken
6	271.5	5.3	1733	S27939	protein-tyrosine p
7	247.5	4.8	348	T40573	auxilin - bovine
8	217.5	4.2	910	S68983	cyclin G-associate
9	217.5	4.2	1305	T31096	probable tyrosine
10	209.5	4.1	434	S5155	glutamate rich pro
11	162	3.1	1271	A45555	hypothetical prote
12	154	3.0	446	T33986	protein FieA4.2 [
13	149	2.9	736	D86271	repeat organellar
14	146.5	2.8	1939	T18372	probable protein-t
15	141	2.7	537	T50099	hypothetical prote
16	140	2.7	981	T03505	giardin - human
17	138.5	2.7	3259	A56539	giardin - human
18	137.5	2.7	3225	I52300	hypothetical prote
19	136	2.6	993	C90072	hypothetical prote
20	136	2.6	1053	S34172	sucrose-phosphate
21	135	2.6	834	D57282	ankyrin-related pr
22	135	2.6	1166	T28680	fibrinogen-binding
23	134.5	2.6	6642	T29757	protein UNC-89 - C
24	133	2.6	264	T25762	hypothetical prote
25	133	2.6	5170	T15348	hypothetical prote
26	132.5	2.6	1244	T19068	hypothetical prote
27	131	2.5	3824	S37431	ankyrin 2, neuroa
28	130.5	2.5	1054	T09833	sucrose-phosphate
29	130.5	2.5	1863	A58881	breast/ovarian can

30	130.5	2.5	1955	2	T30934	myosin-like protei
31	129.5	2.5	786	2	A53939	kinesin homolog KH
32	129.5	2.5	1226	2	S15053	hypothetical prote
33	129	2.5	1871	2	D96796	probable heat shoc
34	128.5	2.5	1195	1	S26722	DNA-directed RNA p
35	128	2.5	1141	2	E89824	hypothetical prote
36	128	2.5	3147	2	T18674	hypothetical prote
37	127.5	2.5	1142	2	S59359	GIN4 protein - yea
38	127.5	2.5	5327	2	T13564	microtubule-associ
39	127	2.5	1507	2	B47328	natural killer cel
40	126.5	2.4	1616	2	G64242	cytadherence-acces
41	126.5	2.4	2039	2	T15347	ankyrin-related un
42	125.5	2.4	2104	2	T38774	myosin-3 heavy cha
43	125	2.4	2722	2	T20532	hypothetical prote
44	125	2.4	427	2	S38002	hypothetical prote
45	125	2.4	790	2	T05576	hypothetical prote

ALIGNMENTS

RESULT 1

T51924

daf-18 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T51924

R:OGG, S.; Ruvkun, G.

Mol. Cell 2, 887-893, 1998

A:Title: The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like metabolic

A:Reference number: Z25864

A:Accession: T51924

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-962 <OGG>

A:Cross-references: EMBL:AF098286; PIDN:AAD03420.1

C:Genetics:

A:Gene: daf-18

Query Match 100.0%; Score 5168; DB 2; Length 962;
Best Local Similarity 100.0%; Pred. No. 1.1e-317;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVTPEPDPVSTSTRSMARDLQENPNRQCEPRVSEPYHNSIVIRIRHIFRTAVSSNRCRT	60
DB	1	MVTPEPDPVSTSTRSMARDLQENPNRQCEPRVSEPYHNSIVIRIRHIFRTAVSSNRCRT	60
QY	61	EYONIDLDCAVITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVKNVNLGGYY	120
DB	61	EYONIDLDCAVITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVKNVNLGGYY	120
QY	121	YDADNFDGNCVCFDMTDHHPSPLELMAPPCEAKEWLEADDKHVIAVHCAGKAGRTGVMI	180
DB	121	YDADNFDGNCVCFDMTDHHPSPLELMAPPCEAKEWLEADDKHVIAVHCAGKAGRTGVMI	180
QY	181	CALLIYINFPSPQILDYSLIIRTKNNKGVITPSQRRYIYYHKLRELNLYPLRMQL	240
DB	181	CALLIYINFPSPQILDYSLIIRTKNNKGVITPSQRRYIYYHKLRELNLYPLRMQL	240
QY	241	IGVYVERPKTWGGSGSKIKVEVNGSGTILFKPDPLIISKSNHQRBRATWLNCCDTPNEPD	300
DB	241	IGVYVERPKTWGGSGSKIKVEVNGSGTILFKPDPLIISKSNHQRBRATWLNCCDTPNEPD	300
QY	301	TGEQKYHGFVSKRAYCFWVPEDAPVFGVDYRIDIREIGFLKKPSDGKIGHVWNTMFAC	360
DB	301	TGEQKYHGFVSKRAYCFWVPEDAPVFGVDYRIDIREIGFLKKPSDGKIGHVWNTMFAC	360
QY	361	DGGLNGGHFEYVDKTPQYIGDDTSIGRKNGMRRNETPMRKIDPDTGNFEFESPWQVNPFG	420
DB	361	DGGLNGGHFEYVDKTPQYIGDDTSIGRKNGMRRNETPMRKIDPDTGNFEFESPWQVNPFG	420
QY	421	LEKHITESQAMENYNYGMIPRYTISKILHEKHKGIVKDDYNDNRKUPMGDKSVTESGK	480
DB	421	LEKHITESQAMENYNYGMIPRYTISKILHEKHKGIVKDDYNDNRKUPMGDKSVTESGK	480

A:Residues: 1-628 <BAR>
A:Cross-references: EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3
A:Note: F3A4.190

Query Match 8.5%; Score 437; DB 2; Length 628;
Best Local Similarity 25.5%; Pred. No. 1e-19;
Matches 156; Conservative 80; Mismatches 195; Indels 180; Gaps 26;

QY 3 TTPDPVSTSTSMARDL---QENNR-----RIRHIFRTAVSSNCRTEYQINIDLDCAVITDR 75
Db 91 SPSPISSSGLSWAKSFQODPNRTDGSMAFRTSELGLHLPTKSGSEVGDSSRS 150
QY 35 -----EPYNSIVE-----RIRHIFRTAVSSNCRTEYQINIDLDCAVITDR 75
Db 151 NTQVGAFESLTKAVVDSRGAVKAMQVKARH-----VSQNKRYQEGEFDLDWYITEN 206
QY 76 IIAIGVPATGI-----EAFNRSKVOTQOFLTRRHGKGNVKNVFNLRGGYYADNPD 127
Db 207 IIAAGPPAGDISSGLFPFEGLYRNHMEVIRKFFETH-KDKYKVNYLCSERLYDASRE 265
QY 128 GNVICFDMTDHPPPSLEMAPCEKAEKLEADDKHVIACHKAGKAGRTGVMICALLIYI 187
Db 266 GKVASPFDDHNCPPQLIPSCQSAITWLKEDIQNVVVVCHKAGMARTGLMICLLLYL 325
QY 188 NFYPSPQRLDYYSIIRTKNNKGVITPSORRYIYYHKLRLERLNLPLR---MOLIGV- 243
Db 325 KFEPTAEAAIDYNNQKCLDGKALVLPQIRVYKYYERVQNGFDGKVPERRGRLNCP 385
QY 244 YVERPPTKVGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTNEFDTGE 303
Db 386 WYIRP-----AITSNHTDLF-----STKHQKTK-----DLGP 415
QY 304 QXVHGFSVKR-AYCFMVPEDAPVF-VEGDVDRIDIREIGFLKFSQKIGHVFNWTFMFA-- 359
Db 416 EDFWIKAPKGVVVFVFAIPGEAGLTLAGDFKIHFD-----SDGDF-YCWLNTLTLDN 467
QY 360 -----CDG-----GLNGHFYV---DKTQP-----YIGDTSIGRKNR 392
Db 468 RTWLKSGDFDGRKRLPAGFHVLEIWPENSPQTSKSDSTQOQSSSSAASSKUK 527
QY 393 RNETPMRKIDPTEGNEFESFQWIVNPPGLEKHITTEQAMENYTNVGMIPRYTISKILHE 452
Db 528 SNEKDDVFSDSGEE-----EGNSQSYSTNEKTASSMHTTSK-PHQ 568
QY 453 KHEKGLVKDNDKRLPMGDKSYTESGKSG-----DIRGVGGPPEIPYKAE 499
Db 569 INEPP-KRDD-----PSANRSVTSSSSSGHYNPINNSLAVSDIKAIA-----ADA 613
QY 500 HVLTFPVYEMD 510
Db 614 SVFSGDEEED 624

RESULT 4
A57075
tensin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-Jul-2000
C:Accession: A57075
R:Chuang, J.Z.; Lin, D.C.; Lin, S.
J. Cell Biol. 128, 1095-1109, 1995.
A:Title: Molecular cloning, expression, and mapping of the high affinity actin-capping protein, tensin, from chicken.
A:Reference number: A57075; MUID:95204530; PMID:7896874
A:Accession: A57075
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11792 <CHU>
A:Cross-references: GB:I06662; NID:g212754; PIDN:AAA73949.1; PID:g212755
C:Superfamily: SH2 homology

F.1520-1629/Domain: SH2 homology <SH2>

Query Match 5.5%; Score 283; DB 2; Length 1792;
Best Local Similarity 20.5%; Pred. No. 2.5e-09;
Matches 172; Conservative 94; Mismatches 252; Indels 322; Gaps 32;

QY 2 VTTPDPVSTSTSMARDLQENPNRQCPGEPRVSEPHNSIVERIHIFRTAVSSNCRTE 61
Db 77 ITKQVDTDP-ATRS-----PRGQARKA-----SRSMSTVATATESC--- 113
QY 62 YQNIIDLCAYITDRIIAGYPATGTEANFRNSKVOTQOFLTRRHGKGNVKNVFNLRGGYY 121
Db 114 -----ELDLVYITERIIAVSYFSTAEQSFNSRLRVAHMLKSKG-DNYVLNL-SERX 167
QY 122 DADNPDGNCVCFDMTDHPPPSLEMAPCEKAEKLEADDKHVIACHKAGKAGRTGVMIC 181
Db 168 DISKLHPKVLDGFWPDLHTPALEKICSICKAMDWLNAAAHNVVLHNGRGLGVVA 227
QY 182 ALLIYINFPSPQRLDYYSIIRTKNNKGVIT--PSQRYIYYHKLRLER--ELNVLPLR 237
Db 228 AYMHYSNISASADQALDRFAMKRFYEDKVVPVQPSQKRYIHVFSGLLSGSIKMNKPLF 287
QY 238 MQ-----LIGVVERPPKTVGGSGKIKVEVNGSTILFKPDPL--- 275
Db 288 LHHVIMHGIPNFPESGCGRPFLKIYQAMQPVVTSIYVNGSQGTGCTIPEGLLKGD 347
QY 276 IISKSNHQRERATWLNCDTNEFDTGQKXHGFSVKRAYCFMVPEDAPVFVEGDVIRDI 335
Db 348 ILLKCYHKKF-----SPTRDVIFRVQFH-----TCAVHDLDI-VFGKEDLDEAF 391
QY 336 REIGFLKFSQ-KGKIGHVFNWTFMPCDGLNGCHGFEYVDKTPYIGDTSIGRKNR 394
Db 392 RD-----ERFPEYKGVFV-----FSY----- 408
QY 395 ETPMCKIDPTEGNEFESFQWIVNPPGLEKHITTEQAMENYTNVGMIPRYTISKILHE 454
Db 409 -----GPEK-----IQGMEHLENGPSVSVDYNTSDPL--- 435
QY 455 EKGIVKDDYNDKRLPMGDKSYTESGKSGDIRGVGGPPEIPYKAEHVLTFPVYEMDRALK 514
Db 436 ---IRWDSYENFNQREDST-----EGTWAEPALPGKHEKVEGHTQGLDGLSY 482
QY 515 SKDLNNGKLVHLRVCVTRDSKMEKSEVFNGLAFHNESTRRLQALTONMKNRPEPCA 574
Db 483 -----AKVKKDSLHSGISGAVNAARPLSA----- 507
QY 575 FGSKGAEMHYPPSVYSSNDGKYNACSENLSVDFEHRNIAVLNRYCYFYKQSTSR 634
Db 508 -----APNHVEHTLSVSDSG-----NSTAST 529
QY 635 RYPRKFRYCLIKKHFIYPADTDDVDENGQPPFH---SPEHYIKQEIKIDAEKAAKGIEN 691
Db 530 KTDR-----TDEPGAPGAPGTHAVLSPE-----EKRELDRLILVGFGLS 568
QY 692 TGPSTSGSAPGTIKKTEASQSDKVKPATEDELPPARLPDNRVRRPVGVDFENPEESC 751
Db 569 APP--MNHAPG-----PA-----PARLP----- 585
QY 752 EHKTVESITAGPEPLEHFLFESYHPNTAGNMLRQDHTDSEVKIARQEAQAFVDQLNGOG 811
Db 586 -----AG--PGRHVVPVPAQVHVNGAGTPL-----LAERETDILDDELFPNODG 624

RESULT 5
A54970
tensin, cardiac muscle - chicken
C:Species: Gallus gallus (chicken)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
C:Accession: A54970; S38330; S21544
R:Lo, S.H.; An, Q.; Bao, S.; Wong, W.K.; Liu, Y.; Janney, P.A.; Hartwig, J.H.; Chen, L.P.
J. Biol. Chem. 269, 22310-22319, 1994
A:Title: Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, expression, and mapping of the high affinity actin-capping protein, tensin, from chicken.
A:Reference number: A54970; MUID:94350987; PMID:8071358

QY 574 AFGSKGAEMHYPPSVRYSSNDKYNACSENLSVDFEHRNIAVLNRYCRYFYKORSTSR 633
Db 461 -----APNVEHTLSVSDSG-----NSTAS 481
QY 634 SRYPRKFRYCLIKKHFIYADTDVDVNDQGFPHFSPHYKEQSKDAEK--AAKGLEN 691
Db 482 TK-----TDRTPGAPGATGHAVALSPERKRDVDRLLVCFGLS 521
QY 692 TQPTSGSSAPOTIKKTEBASQDKVKPATEDLBPAPLPDNRVRFPVGVDFENPEBSC 751
Db 522 AAP--MHNHAPG-----PA-----DARLP----- 538
QY 752 EHKTVESITAGPPLHPLHESYHPNTAGNMLRQDVTSEVKIAEQEAKAFVDQLLNGQ 811
Db 539 -----AG--PGRHVVPQVHVNGAGTPL-----LABRETDLDELNPQDG 577

RESULT 7

T40573

protein-tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40573

R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrall, B.G.

submitted to the EMBL Data Library, January 1999

A:Reference number: Z1938

A:Accession: T40573

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-348 <SEE>

A:Cross-references: EMBL:AL035226; PIDN:CAA22831.1; GSPDB:GN00067

A:Experimental source: strain 972h; cosmid c609

C:Genetics:

A:Gene: SPAC609.02

A:Map position: 2

Query Match 4.8%; Score 247.5; DB 2; Length 348;
Best Local Similarity 33.5%; Pred. No. 3.8e-08;
Matches 65; Conservative 33; Mismatches 87; Indels 9; Gaps 5;

QY 47 HIFRTAVSSNRCTEQVID-----LDCAYITDRIIAIGYPATGTEANFRNSKVQTOQL 101
Db 2 NILRSVVRGRGLQKQKNRSFAVLDVYITTSKVIAMSTPAAGTHKJYRNDLDFVKYL 61
QY 102 TRRHGKGNVKFNL-RGGYYDDADNFDGNVICFDMTDHHPPLSLELMAPPCREAKEWLEAD 160
Db 62 TTQL-KDNWILLNLCAEETVYHLEFKPNVINYQDNPPPLFLWALVNMMDALFQTL 120
QY 161 DKHVIATVCKAGKGTGWICALLIYINFPSPQIOLDYYSIIRTKNNKGVTPSQRYI 220
Db 121 PLLTLVHCKAGKGTGTVICSYLVAFGGL-TAKQSELYTEKRMVRGHGLTISQIRYV 179
QY * 221 VYHKLRERELNYL 234
Db 180 YIEILKQPP-NYL 192

RESULT 8

S68983

auxilin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 08-Oct-1999

C:Accession: S68983

R:Schroeder, S.; Morris, S.A.; Knorr, R.; Plessmann, U.; Weber, K.; Vinh, N.G.; Ungewick

Eur. J. Biochem. 228, 297-304, 1995

A:Title: Primary structure of the neuronal clathrin-associated protein auxilin and its e

A:Reference number: S68983; MUID:95220355; PMID:7705342

A:Accession: S68983

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-910 <SCH>

A:Cross-references: EMBL:U09237; NID:G485268; PIDN:AAA79037.1; PID:G485269

C:Superfamily: dnaJ amino-terminal homology

F:846-910/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 4.2%; Score 217.5; DB 2; Length 910;
Best Local Similarity 21.0%; Pred. No. 1.2e-05;
Matches 211; Conservative 115; Mismatches 371; Indels 307; Gaps 52;

QY 60 TEYNIDLDCAIITDRIIAIGYPATGTEANFRNSKVQTOQLTRRHGKGNVKVFNLRGY 119
Db 54 TSYTKGDLDFYVTSRIIVMSFPLDSVDIGFRNQVDDIRSEFLDSRH-LDHVTYVNLSPKS 112
QY 120 YYDADNPDGIVCFDMTDHHPPLSLELMAPPCREAKEWLEADDKHVIAVHCKAGKGRGTVM 179
Db 113 YRTA-KHRSRVSECSWPIRQAPSLHNLPAVCNRMVNWLLQNPKNVCVHCLDGRAASIL 171
QY 180 ICALLIYINFY--PSPQIOLDYYSIIRTKNNKGVTI-PSORRYIYYHKL---RERELNY 233
Db 172 VGAMFICNLYSTFGPAVRLLY-----AKRPGIGLSPHRRYLGCMCDLADKPYRPHF 225
QY 234 LPLRMQLIGVVVERPPKWTWGGGSKIKEVNGSGTILFKPDPDLIISKSHQERATWLNNC 293
Db 226 KPLTIKISITV-----SPVPFF---NKQR-----NGC 248
QY 294 DTPNEFDTEGOKYH---GFVSKRAYCFMVPEDAPVF-----VEGDVRIIDIRET--- 338
Db 249 RPYCDVLIGETKIYTTCADFERMKEYRV---QDKIFIPLSITVGGDVVVMYHLRSTIG 305
QY 339 -GFLKFSFDGKIGHWNTMF-----ACDGLNGGHFYYVDKTPYIGD 381
Db 306 SRLQAKVNTQIFQLQFHTGFIPLDITVLTKFTKPELDACD-----VPEKYPQLFQ 355
QY 382 DTSIGRKNRMNETPMRKIDPETGNEPESQW-----IVNPPGLEKHITTEQAMENVTN 436
Db 356 VT-----LDVELQPHDKV-----MELTPPEWHYCTKDVNPSILFSSHQHQ--DTLVL 401
QY 437 YGMIP-----PRY-----TISKIL--HEKHEGIVKDDY---NDRKLPWGDKSYTES 478
Db 402 GGOAPIDIPPNPRHFGGGFFSTLCWQDKSEKSFCEEDHAALVNQSESDDELLTSL 461
QY 479 GKSGDIRGVGPPFIY-----KABEHVLITFPVYEMD-----RALSKDLNNGMKLHV 526
Db 462 SPHGNG-----DKPHAARKPSKKQEPAPAPEDVDLLGLEGSAYSKNPFSS----- 510
QY 527 VLRCVDRTRDSKOMKSEVFG-----NLAHF-----NEST-RRIQALQOM 564
Db 511 --PAAPPSNELL--SDLFGGGAAGPVQSGQGVDDVFHPSGPTSTOSTPRRSATSTSA 566
QY 565 NPKYR-PEPCAFGSKGAEMHYPPSVRYSSND--GKYNACSENLSVDFEHRNIAVLNRY 621
Db 567 SPTLRVGEGATDFPGA-----PS-KPSGQDLGSLNTASAS--SDPF----- 607
QY 622 CRYFYKORSTSRSPRFRYCPCLIKKHFIYADTDVDVNDQGFPHF-PEHYIKEQEKI 680
Db 608 ---LQPTFSPTVHASS-----TPAVNIQPDVSGANDWHTKPGF----- 645
QY 681 DAERKAAGIENTGPSTGSS-----APQTIKK-----TEASQSKVKPATEDL--- 724
Db 646 ----GMSKSAATSPGSSHGTPHQNKPTLPDLPADLGLTGGSSFASKPSTPTGLGG 700
QY 725 -PPARLPDNRVRFPVVG-----VDPENPEESCEHKTVESIAGFLEHLPHESY 773
Db 701 FPLSSPKASQSPMGGGWQGGYNNQQTOSKPSMPSHPNQRPN-----YVNSF 753
QY 774 HPNTAGNMLRQDHYTDSVKIAEQEAKAFVDQLLNGQVLQEFMKQKQKVPDNSFADYVT 833
Db 754 SSMFGGQNERKAAANLEGG--OKAADFED-LISGGQ-----FNAHKDK----- 794
QY 834 GQAEVFAQIALBQSEDFORVQNAEVDLHTLGEAFERFHVHVESNGSSKNPKALK 893
Db 795 -----KGPRTIAE-----MRKEEMAKEMDPEKL-----KILEWIEGKERNIRALL 834
QY 894 TREQVVKETGDKTOKTRNHVLLHLEAHRVQIERRETCPHELHPE 937
Db 835 STMHTVLWAGETKWKVPG--MADLVTPQKVKVYKAVLVVHPD 876

RESULT 9

T31096
 cyclin G-associated kinase GAK - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T31096
 R:Kanaoka, Y.; Kimura, S.H.; Okazaki, I.; Ikeda, M.; Nojima, H.
 FEBS Lett. 402, 73-80, 1997
 A:Title: A cyclin G-associated kinase contains a tensin/auxilin-like domain.
 A:Reference number: Z20979; MUID:97165969; PMID:9013862
 A:Accession: T31096
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1305 <KAN>
 A:Cross-references: EMBL:D38560; NID:G1902912; PIDN:BAAL8911.1; PID:G1902913
 A>Note: GAK and cyclin G associate together in vivo
 C:Genetics:
 A:Gene: GAK

Query Match	4.2%	Score 217.5;	DB 2;	Length 1305;
Best Local Similarity	22.1%;	Pred. No. 2.1e-05;		
Matches	92;	Conservative 56;	Mismatches 161;	Indels 107; Gaps 17;

QY 62 YQNIDLCAYITDRIITAIGPATGTEANFRNSKVQTOQLTRRHGKGNVKNLGGVYY 121
 DB 401 YAKGDLDISYITSRIAIVMSFPAEGVESAIKNINIEDVRLFLDAKH-PGHVAVYNL-SPRIY 458

QY 122 DADNFDGNVICFDMTDHPPSLMAPPFCREAKEWLEADDKHVIACHKAGKGRGTVMIC 181
 DB 459 RASKFNRVTECGWAVRRAPHLHSLYTLCSRHAWLREDRNVCVCHMDGRAASAVVC 518

QY 182 ALLIYINFPSPRQILDYYSIIRTKNNKGVTTIPSORRYIYYHKLRELYNLPLRMQI 241
 DB 519 AFLCFCLRFSTAAAVYMFMSKRC- PGIW-PSHKRYIEY-----VC 558

QY 242 GYVVERPPKTTGGGKIKVEVNGSTILFKPDPLIISKNSHOR-----BRATLNN 292
 DB 559 DMVAEPIPTHKPLVK-----SVNTPVLPFSKQNRGCRPFCEVYVGBERV- 607

QY 293 CDTNPFDDTGEOKYHGFVSKRAVCEWVPEDAPVF-----VEGDVIRIDREI-----GFLK 342
 DB 608 -TTSQBYDMKE-----FKIEDGKAVIPGIVQGDVLTIIYHASTIGGRQ 654

QY 343 -RPSDGKIGHVWNTMF-----ACDGLNGGHFEYVDKTPQYIGDDTSI 385
 DB 655 AKMASMKFQIQPHTGFVPRNATTVKFAKYDLDAKD-----IQEKYP---DLFQV 701

QY 386 GRKNGMRNETPWRKIDPETGNEFSPWQIVNPPGLEKH-----TERQAMENTNYG 438
 DB 702 NLEVEVEPRDRPSRDV-----PPWENTSRLGRLNPKILFSNRBEQDDILSKFG 748

RESULT 10

S55155
 probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: probable tyrosine phosphatase N1220; protein JTB434; protein N1872
 C:Species: Saccharomyces cerevisiae
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S55155; S59260; S63073
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 submitted to the EMBL Data Library, November 1994
 A:Description: A 43.5 kb fragment of the chromosome XIV.
 A:Reference number: S55136
 A:Accession: S55155
 A:Molecule type: DNA
 A:Residues: 1-434 <NAL>
 A:Cross-references: EMBL:Z46843; NID:G861113; PID:G854509
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 Yeast 11, 1195-1209, 1995
 A:Title: A 43.5 kb segment of yeast chromosome XIV, which contains MPA2, MEP2, CAP/SRV2,
 A:Reference number: S59241; MUID:96109932; PMID:8619318

A:Accession: S59260
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-434 <MAW>
 A:Cross-references: EMBL:Z46843; NID:G861113; PIDN:CAA86897.1; PID:G854509
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63069
 A:Accession: S63073
 A:Molecule type: DNA
 A:Residues: 1-434 <MAP>
 A:Cross-references: EMBL:Z71404; NID:G1302063; PID:e2339804; PID:G1302064; MIPS:YNL128w
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:TEP1
 A:Cross-references: SGD:S0005072; MIPS:YNL128w
 A:Map position: 14L
 C:Keywords: transmembrane protein
 F:38-54/Domain: transmembrane #status predicted <TM1>

Query Match	4.1%	Score 209.5;	DB 2;	Length 434;
Best Local Similarity	23.8%;	Pred. No. 1.3e-05;		
Matches	91;	Conservative 44;	Mismatches 146;	Indels 101; Gaps 15;

QY 67 LDCAYITDRIITAIGYPA-TGTEANFRNSKVQTOQLTRRHGKGNVKNLGGVYY 121
 DB 42 LDISYILVNLVCSYPVNTYPKLLYRNSLDDLLILFTVYHKGNGFRIFNFKGKEDSDYK 101

QY 122 DAD-----NFD-----GNVIC--FDMTD 137
 DB 102 DNDLIGIAAKFESKDFEQLRSTLINDGKIPIPIDLRTLTVEETNNVICERIGWLD 161

QY 138 HPPSLEMAPFCREAKEWLEADDKHVIACHKAGKGRGTVMICALLI-YNFYVSPRQI 196
 DB 162 HFPFPELLEIIVDGIENYLSVSKNRVAVLHCRMGKGRSGMITVAYLMKYLQCPGLEARL 221

QY 197 LDYYSIIRTKNNKGVTTIPSORRYIYY-----HKLRELYNLPLRMQLIGYVVERPPKT 251
 DB 222 IFMQARFYKGTNGVTIPSQLRYLRYHEFFITHEKAAQE-----GISNE----- 265

QY 252 WGGGSKIKEVGVNGSTILFKPDPLIISKNSHORERATLNNCDTNPEDTGEOKYHGFVS 311
 DB 266 ---AVKFKFKELAKWTFRLRSSLTSSAIVTTKIQHYN--DORNALLTRKVVYSDIMA 320

QY 312 KRA---YCFMVPEAPVFEVGDVIRIDREIIGFLKKFSDGKI-----GHVWNTWTFACDG 362
 DB 321 HECGGMVTFIFGRDY-LTLENDCRIF-TLGTSKSKAASSIISWTSCASCWLN----- 372

QY 363 GLNGHGFYVDKTPYIGDDTS 384
 DB 373 -----YLETLMHIIKDDSS 386

RESULT 11

A45555
 glutamate rich protein - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000
 C:Accession: A45555; S27831
 R:Barre, M.B.; Dziegiel, M.; Hough, B.; Petersen, E.; Rieneck, K.; Riley, E.; Meis, J.F.; J.
 Mol. Biochem. Parasitol. 49, 119-131, 1991
 A:Title: Primary structure and localization of a conserved immunogenic Plasmodium falciparum life cycle.
 A:Reference number: A45555; MUID:92131041; PMID:1775153
 A:Accession: A45555
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1271 <BOR>
 A:Cross-references: EMBL:M59706; NID:G160311; PID:G160312
 A>Note: sequence extracted from NCBI backbone (NCBI:77801, NCBIP:77802)

[illegible]

A:Molecule type: DNA
A:Residues: 1-736 <STO>
A:Cross-references: GB:AE005172; NID:98778384; PIDN:AAF79392.1; GSPDB:GN00141
C:Genetics:
A:Gene: F16A14.2
A:Map position: 1

Query Match 2.9%; Score 149; DB 2; Length 736;
Best Local Similarity 20.3%; Pred. No. 0.19;
Matches 150; Conservative 102; Mismatches 260; Indels 228; Gaps 39;
QY 218 RYIVYVHLKRLER-----ELNVLPLRMQLIGVYVERPKTWGGGSKIYVEVNGSTILF 270
DB 77 RYWKYLRPRPRPSPTSDVSLP-KSEFTGKW-KSTLSITTEGEFFITE-NSSSPHIV 133
QY 271 KPDPLIISKNSHQREATWLNCDTNEFDTEGEQVHGFVSKRAYCFMVPEADAPVFEVD 330
DB 134 KAEPKFVSGDGRSGEERLKFSDKDPDFSFNEDKSY-----PAKRPLCLVSGA 181
QY 331 VRID--IREIGFLKKE-----DGKIGHVWNTMFACDGLNGHPEY 371
DB 182 KEGDEPVQIRIGLSHGASFAPTYVQKLVSLGAGNGDQMYVHPW-----KGLANMKRTF 234
QY 372 VDKTPYIGDDTSIGRKGMRNETPMRKIDP-----ETG---NEFESPMQIVNPPGL 421
DB 235 NEKTRYAGESGSKIREDLIKGFNP-HKVTPLWNGRLGFTGFAIVDFGKEW-----285
QY 422 EXHITEBOAMENYNYGMIPPRYTISKILHEKH-----KGIV--KDYNDRKLP 470
DB 286 -----EGFRNATMFKHFEVSQCGKRDHLTRDPGDKLYGWVAKQDDYYSR-TAI 334
QY 471 GDSYTESGSGDIRGVGPFPIPYKAEHVLTFP-VYEMDRALKSKDLNNGKMLHVLR 529
DB 335 GD-----HLRKQGDLSVSGK-----BAEDQRKFTLVSNLENTLVTKSDNLOQMESIYKQ 385
QY 530 CVDTRDSKMKSEVFGNLAFLHNESTRRLQALTMNPKWRPPEPCAFSGKGAEMHYPPSVR 589
DB 386 TSVLEKRMKEKDEMINT--HNEKMSIMQOTAR-----DYLASI- 422
QY 590 YGSNDGKYNGACSENILVDPFFEHNRNIAVLNRYCRYFYKORSTSRYP-RKFRYCPLIKK 648
DB 423 YEEHE-----KASQHLAQRKEYED-----RENYDKCAQAKTERRKLQW---QK 465
QY 649 HFVIPADTDDVDENGQPFPHSBEHYKE-----QEKIDAEKAAK-----CI 689
DB 466 HKNLMA-TOQNKADEMMRLABQOQREKDELKQVRELEKTDABQALBELIERMRGDL 524
QY 690 ENTGPSTGSSAPGTIK---KTEASQSK-----VKPA-TEDELPPAR- 728
DB 525 QVNGHMQEGEGEDSKIKEMIEKTEKEEDWEYQESLYQTLVYKHGYTNDLQDARK 584
QY 729 -LPDNYRFPV-----VGVDNFENPEESCEHK--TVESIAGFPEPL-----EHLFHES 772
DB 585 ALIRSMRELTTRAYIGVKRMGALDETFFKKVAKEYPAVEADKABELCSLWEEHLGDSA 644
QY 773 YNPNTAGNMLRDYHTDSEVKAQAEKAFVDOLLNGQGVLFQPMQKVPVSDNSPADYV 832
DB 645 WHP-----IKVVEKDGLA-KEELNEEDELQELRKL-----675
QY 833 TGOAEVFKAQIALLEQSEDF 852
DB 676 -GE-EVYAAVTQALKERNEY 693

RESULT 14
T18372
repeat organellar protein - Plasmodium chabaudi
C:Species: Plasmodium chabaudi
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18372
R:Werner, E.B.; Taylor, W.R.; Holder, A.A.
Mol. Biochem. Parasitol. 94, 185-196, 1998
A:Title: A Plasmodium chabaudi protein contains a repetitive region with a predicted sp

A:Reference number: Z18922; MUID:98418765; PMID:9747969
A:Accession: T18372
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1939 <WER>
A:Cross-references: EMBL:U43145; NID:g1151157; PID:g1151158; PIDN:AAC63403.1

Query Match 2.8%; Score 146.5; DB 2; Length 1939;
Best Local Similarity 18.5%; Pred. No. 1.1;
Matches 180; Conservative 152; Mismatches 368; Indels 273; Gaps 43;
QY 86 IEAFNRNSKVQTOFLTRRHGKGNVKNFNLGRGGYVYDADNFDGNVICFDMTDHHPSPSLEL 145
DB 144 LNLNKENKINKEITL--KREKLNIDIESEYI--EKNKEKEKLNVEVI-NIKMSLDK 197
QY 146 MAPFCREAKLEWLEADKHVIAVHCAGKRGTVGMICALLIYINFPSPQRLDDYYSIIRT 205
DB 198 LTCVEQEKDNLKINKKVIKENNLRELK-----EPMKEKEIEI--SLDGT 243
QY 206 KNNK-----GVTPISQRRYIYY--HKLRERELNYLPLRMQLIGVYVERPPKTWGGGSK 257
DB 244 INDKNAYEKELEIFSEKRGKMIEMLDKLEKENF-----279
QY 258 IKVEVNGSTILFKPDPPLIISKNSHQREATWLNCDTNEFDTEGEQKYHGF-----309
DB 280 -----ANKQAKLEKENEIIIIEKLDIESR-----EKDFKSEKEEFASMENELTLK 325
QY 310 --VSKRA-----YCFMVPEDAPVFEVDVRIDIRIGFLKPKPSGDKIGHVWNTMFACDG 362
DB 326 SDSLKNACQMEVYKLEIKDLSQSLVEKE-----REIFEIKNEYDDKINNMKEKLSSINDK 380
QY 363 GLNGCHFYVKTOPYIGDDTSIGRKGMRNETPMRKIDPDTGNEFESPMQIVN--PPG 420
DB 381 G-----IDNTVLH--SEEEKINKL--LKEKETELNEIHKYKYNLEIETIKNELKEKEEE 429
QY 421 LEK-----HITE-----EOAMENYNYGMIPPRYTISKILHEKHEKGIKVD 461
DB 430 LEKNKAHTVEVNTLKEIKLEKTEDEKKEGHN-----ELNENLQSLKLEKED 481
QY 462 DYNDRKLPMDGKSYTESGSGDIRGVGPFPIPYKAEHVLTFPYVYEMDRALKS-KDLNN 520
DB 482 NIKNENTELNDKISS-----LNSEVNILNKDKQTLGNDIKTLNDLIN 523
QY 521 GKMLHVLRCDVTRDSKMKSEVFGNLAFLHNESTR-RLQALTMNPKWRPPEPCAFSGSK 579
DB 524 NLKNE-----INTSNKKNKMK-----DLAMLENEWEGKCVVIDETEKYKKEIFMLESK- 574
QY 580 AEMHYPPSVRYSSNDGKYNAGCS--ENLV-----SDFFEHRNIAVLNRYCRYFYK 627
DB 575 -----LKEKENVADLNDEISILRNSIYVKEKEFIEMKEFYENK----INLPKNFTEE 622
QY 628 QR-----STSRSRYPKRYCPYLIKKHFIYIPADTDDVDENGQPFPHSBEHYKEQB-- 678
DB 623 KKNYIENELNSURLKYDNE--QGLIKQ-----IDELNIQKLKTEEKYLQLYNDN 669
QY 679 -----KIDAEKAAKGIENGTGSSSAPGTIKKTEASQSKDKVPATEDELPAPRL 729
DB 670 MHMFRSICTKIDMPYS-----ENIKGSDLVDFVTAYIKRRDESSSDANPDTHKEN----V 721
QY 730 PDNVRFPVGVDFENPEESCE-----HKTVESTAGFEPLH-LFHESYHPNTA----- 778
DB 722 AELEKGAHAAIVAELEBEKHEETAKLGECHKEVVLRLGQHKHEETILEKHKDVVTKLGE 781
QY 779 ---GNMLR-QDYHTDSEVKIAEQ-----EAKAFVDQLLNGGVLOEFMKQKFKVPSD 825
DB 782 QHKENIIKLEBEHKDVVTKLGDQYKEETAKLKEEHAVVVAELEEKHLGEGHEKEMVDELE 841
QY 826 NSFADYVTVQAEVFKAQIALLEQSEDFQFVQANAEVDLEHT-----LG 869
DB 842 KKHADFVGLGEKHKHKAETAKLEEGH-----KSEMNVEKRRHADFVEGLEEKHKHAKTAKLG 896
QY 870 EAF-----ERFGHVVEESNGSSKNPKALKTRQOMVKETGDKTQKTRNHYLLHLEAHN 921

Db 897 EGHREVVAGLEEKHEVVAEL--EEKKEEIAKLEEGHKEVMAELGEKHEKVAGLEAKH 954

QY 922 RVOIERRETCPPEL 934

Db 955 NLEEGHKEMVAEL 967

RESULT 15

T50099
probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C:Accession: T50099

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.

submitted to the EMBL Data Library, February 2000

A:Reference number: Z25037

A:Accession: T50099

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-537 <WOO>

A:Cross-references: EMBL:AL158056; PIDN:CAE76271.1; GSPDB:GN00066; SPDB:SPAC1782.09c

A:Experimental source: strain 972h(-); cosmid c1782

C:Genetics:

A:Gene: SPDB:SPAC1782.09c

A:Map position: 1

A:introns: 17/1

Query Match 2.7%; Score 141; DB 2; Length 537;

Best Local Similarity 24.6%; Pred. No. 0.38;

Matches 70; Conservative 47; Mismatches 85; Indels 82; Gaps 16;

QY 37 YNSIVERIRHIFRTAVSSNRCTEYQNIDL-----DCAYITDRIIAIGYPAT 84

Db 142 YYITIQDCVYGLWRARESS---ILNIRNDVHDYETVERVENGDFNWSPKETAFASP-- 196

QY 85 GIEANFRNSKVOTQ-----FLTRHKGKGVKVNLRGGYYVDADNFDGNV--- 130

Db 197 -IQAGWNHASTRPKLPQPAIVLDYFVANK-----VKLIVRLNGPLDYDKKTFE-NVGIR 249

QY 131 ---ICFDMTDHPPPSLELMAPFCREAKWL---EADDKHVIHVCKAGKGRGTGMICAL 183

Db 250 HKEMYFE--DGVPELSLV-----KEFIDLTEEVEDGVIAVCKAGLGRGTGCLIGAY 300

QY 184 LIYINFPSPQILDYYSIIRTKNNKGVITPSQRYI-----YYVHKLRERELNYL 234

Db 301 LIYKHCFTANEVIAVMRMR---PGWVVGQOHLHINQVHFRAIFYEKAMGRAIQQA 355

QY 235 PLRMQLIGYVVERPPK-----TWGGGSKIKVEVNGSGTILFKPDP 274

Db 356 TAAEPL-----ATPPRHPLNATNGTSQ-----SNISTPLPEPTP 389

Search completed: December 10, 2003, 20:35:04

Job time : 32.8035 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:57 ; Search time 16.5821 Seconds
(without alignments)
2711.873 Million cell updates/sec

Title: US-09-205-658A-310

Perfect score: 5168

Sequence: 1 MVTPTDVPDSTRSMARDL.....IAHFSNFSFSDSNFDQAIYL 962

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490.5	9.5	403	1 PTEN HUMAN	O00633 homo sapien
2	490.5	9.5	403	1 PTEN MOUSE	O08586 mus musculu
3	333.5	6.5	551	1 TPTN_HUMAN	P56180 homo sapien
4	282	5.5	1744	1 TENS_CHICK	O04205 gallus gall
5	217.5	4.2	910	1 AUX1_BOVIN	Q27974 bos taurus
6	217.5	4.2	1305	1 GAK RAT	P97874 rattus norv
7	209.5	4.1	434	1 YNM6 YEAST	P53916 saccharomyc
8	206	4.0	1311	1 GAK_HUMAN	O14976 homo sapien
9	141	2.7	537	1 FLPI_SCHPO	Q9p7hl schizosacch
10	138.5	2.7	3259	1 GIAN_HUMAN	Q14789 homo sapien
11	136	2.6	1053	1 SPS_SOLITU	Q43845 solanum tub
12	134.5	2.6	6632	1 UN89 CAEEL	O01761 caenorhabdi
13	133	2.6	264	1 YLPK CAEEL	P91301 caenorhabdi
14	132.5	2.6	1244	1 YP83 CAEEL	Q09441 caenorhabdi
15	131	2.5	3524	1 ANK2_HUMAN	Q01484 homo sapien
16	130.5	2.5	1054	1 SP51 CRAPL	O04932 cratereostig
17	130.5	2.5	1863	1 BRCl_HUMAN	P38398 homo sapien
18	130.5	2.5	1955	1 PUMA_PARUN	O61308 parascaris
19	129.5	2.5	786	1 FL10_CHLRE	P45869 chlamydomon
20	129.5	2.5	1226	1 YCS3 YEAST	P25357 saccharomyc
21	128.5	2.5	1195	1 RPOB_THEAC	Q03587 thermoplasm
22	127.5	2.5	1142	1 GIN4 YEAST	Q12263 saccharomyc
23	127	2.5	1453	1 NKCR MOUSE	P30415 mus musculu
24	126.5	2.4	1616	1 P200_MYCGE	Q49429 mycoplasma
25	125.5	2.4	2104	1 MY53_SCHPO	O14157 schizosacch
26	125	2.4	427	1 EBP2 YEAST	P36049 saccharomyc
27	125	2.4	5596	1 MDN1_HUMAN	Q9nu22 homo sapien
28	124.5	2.4	1959	1 MYH9 CHICK	P14105 gallus gall
29	124.5	2.4	4344	1 DYHC_EMENI	P45444 emericeila
30	124	2.4	1129	1 EG27 CAEEL	Q09228 caenorhabdi
31	124	2.4	1267	1 DHR1 YEAST	Q04217 saccharomyc
32	123.5	2.4	796	1 PRH_ARATH	P48785 arabidopsis
33	123.5	2.4	1063	1 CDCE CAEEL	P81299 caenorhabdi

34 123 2.4 660 1 SYM_BACHD O9kgk8 bacillus ha
35 121.5 2.4 1183 1 RMS1_YEAST Q08965 saccharomyc
36 121.5 2.4 1216 1 PIB1 RAT P10687 rattus norv
37 121.5 2.4 2869 1 RBP1_PLAVB Q00798 plasmodium
38 121 2.3 1027 1 EB30 CAEEL P34441 caenorhabdi
39 120.5 2.3 1208 1 PCP1_SCHPO Q92351 schizosacch
40 120.5 2.3 1216 1 PIB1_BOVIN P10894 bos taurus
41 120.5 2.3 1940 1 MYH3_HUMAN P11055 homo sapien
42 120 2.3 595 1 REB1_KLUJA Q05950 kluyveromyc
43 119.5 2.3 710 1 LT78 ARATH Q06738 arabidopsis
44 119.5 2.3 1233 1 CIBC_BACTM Q45774 bacillus th
45 119 2.3 770 1 ACE2_YEAST P21192 saccharomyc

ALIGNMENTS

RESULT 1
PTEN_HUMAN
ID PTEN_HUMAN STANDARD; PRT; 403 AA.
AC O00633; O02679;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1 OR TEP1.
OS Homo sapiens (Human), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9615;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX SPECIES=Human, and C.familiaris;
RA STECK P.A., Pershouse M.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattiger T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.,
RA "Identification of a candidate tumour suppressor gene, MMAC1, at
chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Rodgers L., Bigner S.H., Giovannella B.C.,
RA Miliareis C., Liaw D., Podsypanina K., Bose S., Wang S.L., Puc J.,
RA Ittmann M., Tycko B., Hibshoosh H., Wigler M.H., Parsons R.;
RA "PTEN, a putative protein tyrosine phosphatase gene mutated in human
brain, breast, and prostate cancer.";
RL Science 275:1943-1947(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA MEDLINE=97330649; PubMed=9187108;
RA Li D.M., Sun H.;
RA "TEP1, encoded by a candidate tumor suppressor locus, is a novel
protein tyrosine phosphatase regulated by transforming growth factor
beta.";
RL Cancer Res. 57:2124-2129(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA Wang S., Li J., Liaw D., Bose S., Podsypanina K., Parsons R.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA Jensen K., de la Bastide M., Parsons R., Parnell L.D., Dedhia N.,
RA Gottesman T., Gnoj L., Kaplan N., Lodhi M., Johnson A.F., Shohdy N.,
RA Hasegawa A., Haberman K., Huang E.N., Schutz K., Calma C., Granat S.,
RA Wigler M., McCombie W.R.;

RT "Genomic sequence of PTEN/MMAC1.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Gray N.B., Stewart L.M.D., Hamilton J.A., Roberts K.G., Watson G.,
 RA Snary D.;
 RA "Genomic sequence of chromosome 10q23.3 containing exons 6, 7, 8 and 9
 RT of the PTEN gene.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Tissue=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP CHARACTERIZATION.
 RC SPECIES=Human;
 RX MEDLINE=97404346; PubMed=9256433;
 RA Myers M.P., Stolarov J.P., Eng C., Li J., Wang S.I., Wigler M.H.,
 RA Parsons R., Tonks N.K.;
 RT "p-TEN, the tumor suppressor from human chromosome 10q23, is a dual-
 RT specificity phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9052-9057(1997).
 RN [9]
 RP FUNCTION.
 RC SPECIES=Human;
 RX MEDLINE=98256248; PubMed=9593664;
 RA Maehama T., Dixon J.E.;
 RT "The tumor suppressor, PTEN/MMAC1, dephosphorylates the lipid second
 RT messenger, phosphatidylinositol 3,4,5-trisphosphate.";
 RL J. Biol. Chem. 273:13375-13378(1998).
 RN [10]
 RP PHOSPHORYLATION OF THR-366; SER-370 AND SER-385.
 RC SPECIES=Human;
 RX MEDLINE=2233751; PubMed=12297295;
 RA Miller S., Lou D., Seidman D., Iane W., Neel B.;
 RT "Direct identification of PTEN phosphorylation sites.";
 RL FEBS Lett. 528:145-145(2002).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.10 ANGSTROMS) OF 7-353.
 RC SPECIES=Human;
 RX MEDLINE=20021619; PubMed=1055148;
 RA Lee J.-O., Yang H., Georgescu M.-M., Di Cristofano A., Maehama T.,
 RA Shi Y., Dixon J.E., Pandolfi P., Pavletich N.P.;
 RT "Crystal structure of the PTEN tumor suppressor: implications for its
 RT phosphoinositide phosphatase activity and membrane association.";
 RL Cell 99:323-334(1999).
 RN [12]
 RP VARIANT CD ASN-137 INS.
 RC SPECIES=Human;
 RX MEDLINE=98007985; PubMed=9345101;
 RA Tsou H.C., Teng D.H.-F., Ping X.L., Brancolini V., Davis T., Hu R.,
 RA Xie X.X., Gruener A.C., Schrager C.A., Christiano A.M., Eng C.,
 RA Steck P., Ott J., Tavtigian S.V., Peacocke M.;
 RT "The role of MMAC1 mutations in early-onset breast cancer: causative
 RT in association with Cowden syndrome and excluded in BRCA1-negative
 RT cases.";
 RL Am. J. Hum. Genet. 61:1036-1043(1997).
 RN [13]
 RP VARIANTS CD GLU-343 AND LEU-347.
 RC SPECIES=Human;
 RX MEDLINE=98153621; PubMed=9399897;
 RA Lynch E.D., Ostermeyer E.A., Lee M.K., Arena J.F., Ji H., Dann J.,
 RA Swishelm K., Suchard D., MacLeod P.M., Kvinnelsland S., Gjertsen B.T.,
 RA Heimdal K., Lubs H., Moeller P., King M.-C.;
 RT "Inherited mutations in PTEN that are associated with breast cancer,
 RT Cowden disease, and juvenile polyposis.";
 RL Am. J. Hum. Genet. 61:1254-1260(1997).
 RN [14]
 RP VARIANTS CD ARG-123 AND ARG-124.
 RC SPECIES=Human;
 RX MEDLINE=97402224; PubMed=9259288;
 RA Neelen M.R., van Staveren W.C.G., Peeters E.A.J., Ben Hassel M.,
 RA Gorlin R.J., Hamm H., Lindboe C.F., Frys J.-P., Sijmons R.H.,
 RA Woods D.G., Mariman E.C.M., Padberg G.W., Kremer H.;
 RT "Germline mutations in the PTEN/MMAC1 gene in patients with Cowden
 RT disease.";
 RL Hum. Mol. Genet. 6:1383-1387(1997).
 RN [15]
 RP VARIANT CD GLU-129.
 RC SPECIES=Human;
 RX MEDLINE=97285123; PubMed=9140396;
 RA Liaw D., Marsh D.J., Li J., Dahia P.L.M., Wang S.I., Zheng Z.,
 RA Bose S., Call K.M., Tsou H.C., Peacocke M., Eng C., Parsons R.;
 RT "Germline mutations of the PTEN gene in Cowden disease, an inherited
 RT breast and thyroid cancer syndrome.";
 RL Nat. Genet. 16:64-67(1997).
 RN [16]
 RP VARIANT BZS ARG-170.
 RC SPECIES=Human;
 RX MEDLINE=97382333; PubMed=9241266;
 RA Marsh D.J., Dahia P.L.M., Zheng Z., Liaw D., Parsons R., Gorlin R.J.,
 RA Eng C.;
 RT "Germline mutations in PTEN are present in Bannayan-Zonana syndrome.";
 RL Nat. Genet. 16:333-334(1997).
 RN [17]
 RP VARIANT CD GLU-289.
 RC SPECIES=Human;
 RX MEDLINE=99014194; PubMed=9797362;
 RA Chi S.-G., Kim H.-J., Park B.-J., Min H.-J., Park J.-H., Kim Y.-W.,
 RA Dong S.-H., Kim B.-H., Lee J.-I., Chang Y.-W., Chang R., Kim W.-K.,
 RA Yang M.-H.;
 RT "Mutation abrogation of the PTEN/MMAC1 gene in gastrointestinal
 RT polyps in patients with Cowden disease.";
 RL Gastroenterology 115:1084-1089(1998).
 RN [18]
 RP VARIANTS CD HIS-68 AND PRO-112.
 RC SPECIES=Human;
 RX MEDLINE=98260873; PubMed=9600246;
 RA Tsou H.C., Ping X.L., Xie X.X., Gruener A.C., Zhang H., Nini R.,
 RA Swishelm K., Sybert V., Diamond T.M., Sutphen R., Peacocke M.;
 RT "The genetic basis of Cowden's syndrome: three novel mutations in
 RT PTEN/MMAC1/TEP1.";
 RL Hum. Genet. 102:467-473(1998).
 RN [19]
 RP VARIANTS CD AND BZS.
 RC SPECIES=Human;
 RX MEDLINE=98133933; PubMed=9467011;
 RA Marsh D.J., Coulon V., Lunetta K.L., Rocca-Serra P., Dahia P.L.M.,
 RA Zheng Z., Liaw D., Caron S., Duboue B., Lin A.Y., Richardson A.-L.,
 RA Bonnetblanc J.-M., Bressieux J.-M., Cabaret-Moreau A., Chompert A.,
 RA Demange L., Beles R.A., Yahanda A.M., Fearon E.R., Fricker J.-P.,
 RA Gorlin R.J., Hodgson S.V., Huson S., Lacombe D., Leprat F., Odent S.,
 RA Toulouse C., Olopade O.I., Sobol H., Tishler S., Woods C.G.,
 RA Robinson B.G., Weber H.C., Parsons R., Peacocke M., Longy M., Eng C.;

Query Match 9.5%; Score 490.5; DB 1; Length 403;
Best Local Similarity 31.3%; Pred. No. 1.1e-22;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCTEYQNIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62

QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E M A P F C R A K E W L E A D D K H V I A V 167
DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I V I N F Y P S P R Q I L D Y I S I R T K N K N G V T I P S O R R Y I Y Y H K L R 227
DB 123 H C K A G K G R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H R E R A 287
DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
DB 235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K Q N K M L K K - - 267

QY 346 D O K I G H V W F N T M F - - - - - A C D G G L N G - G H F E V D K T Q P V I G D T S I G R K N 389
DB 268 - D K M F H F W N T F I P G P E E T S E K V E N G S L C Q E I D S I C S I E R A D N D K E Y L - - - - - 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 2
ID PTEN_MOUSE STANDARD; PRT; 403 AA.

AC 008586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Pershouse M.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattier T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.,
RT "Identification of a candidate tumour suppressor gene, MMAC1, at
chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
CC 1- FUNCTION: Potential tumor suppressor. Acts as a phosphoinositide
CC 3-phosphatase by regulating PtdIns(3,4,5)P3 levels.
CC H(2)O = phosphatidylinositol-3,4,5-trisphosphate +
CC -!- COFACTOR: Magnesium.
CC -!- PTM: Phosphorylation results in an inhibited activity towards
CC PIP3 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -!- SIMILARITY: Contains 1 tensin domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U92437; AAC53118.1; -;
DR MGI; 109583; Pten.
DR GO; GO:0016506; F:apoptosis activator activity; IMP.
DR GO; GO:0016334; F:phosphatidylinositol-3,4,5-trisphosphate 3-...; IDA.
DR GO; GO:0016477; P:cell migration; IMP.
DR GO; GO:0007417; P:central nervous system development; IMP.
DR GO; GO:0006917; P:induction of apoptosis; IMP.
DR InterPro; IPR000387; TYR phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW Hydrolase; Anti-oncogene; Phosphorylation.
FT DOMAIN 22 303
FT ACT_SITE 124 124
FT MOD_RES 366 366
FT MOD_RES 370 370
FT MOD_RES 385 385
SQ SEQUENCE 403 AA; 47152 MW; 75F97C3DD6843BA9 CRC64;

Query Match 9.5%; Score 490.5; DB 1; Length 403;
Best Local Similarity 31.3%; Pred. No. 1.1e-22;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCTEYQNIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62

QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E M A P F C R A K E W L E A D D K H V I A V 167
DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K G R T G V M I C A L L I V I N F Y P S P R Q I L D Y I S I R T K N K N G V T I P S O R R Y I Y Y H K L R 227
DB 123 H C K A G K G R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H R E R A 287
DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V I Y S N S G P T R R - 234

QY 288 T W L N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
DB 235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K Q N K M L K K - - 267

QY 346 D O K I G H V W F N T M F - - - - - A C D G G L N G - G H F E V D K T Q P V I G D T S I G R K N 389
DB 268 - D K M F H F W N T F I P G P E E T S E K V E N G S L C Q E I D S I C S I E R A D N D K E Y L - - - - - 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 3
ID TPTE_HUMAN STANDARD; PRT; 551 AA.

AC P56180;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative protein-tyrosine phosphatase TPTE (EC 3.1.3.48).
GN TPTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20065863; PubMed=10598804;
RA Chen H., Rossier C., Morris M.A., Scott H.S., Gos A., Bairoch A.,
RA Antonarakis S.E.;

"A testis-specific gene, TPTE, encodes a putative transmembrane tyrosine phosphatase and maps to the pericentromeric region of human chromosomes 21 and 13, and to chromosomes 15, 22, and Y.";
Hum. Genet. 105:399-409(1999).
(2)
SEQUENCE FROM N.A.
RT MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramer J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
CC -!- FUNCTION: COULD BE INVOLVED IN SIGNAL TRANSDUCTION.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN TESTIS.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007118; AAC34574.1; -;
DR EMBL; AL163201; CAB90528.1; -;
DR Genew; HGNC:12023; TPTE.
DR MIM; 604336; -;
DR GO; GO:0016021; C-integral to membrane; TAS.
DR GO; GO:0006470; P-protein amino acid dephosphorylation; TAS.
DR GO; GO:0007165; P-signal transduction; TAS.
DR InterPro; IPR005820; M-channel nlg.
DR InterPro; IPR000387; TYR phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase; Transmembrane.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT DOMAIN 236 518 TENSIN.
FT ACT_SITE 338 338 POTENTIAL.
FT CONFLICT 386 386 E -> K (IN REF. 2).
FT CONFLICT 470 470 P -> L (IN REF. 2).
SQ SEQUENCE 551 AA; 64307 MW; 39C031C7D30685D2 CRC64;
Query Match
Best Local Similarity 31.5%; Score 333.5; DB 1; Length 551;
Matches 75; Conservative 51; Mismatches 95; Indels 17; Gaps 4;
QY 41 IVERINHIF-----RTAVSSNRCRTEYQNIDLCAYITDRIIAGYPATGIEANF 90
DB 201 ILLRIFLPHQKLEKLRVSEKRRVTRDGDPLDLYTYTERIAMSFPSSGRQSPY 260
QY 91 RNSKVQTQQLFTRHCKGNKVFNLGGYYVDADNFGNVICFDMTDHHPSPLELWAPFC 150
DB 261 RNPKEVVRFLDKKH-RNHYVYNLCSEAYDPKPHNVRVIMDDHNVPTLHQKVVPT 319
QY 151 REAKEWLEADKHVIAVHCAGKRGTVGMICALLIYVFPSPQLDLYSIIRTKNN-- 208

DB 320 KEVNEWMAQDLNIVAIHCKGTDRTGTWCAFLIASICSTAKESLYYFGERRDKTHS 379
QY 209 ---KGVTPSORRYIYYHKLRE-RELNYLPLRQOLIGVYVERPKTWGGSKIKVEV 262
DB 380 EKFOGVETPSQKRYVAYFAQVKHLYNNWLPRLFIKHFIIYSIPRYVRDLKIQIEM 437
RESULT 4
TENS_CHICK
ID TENS_CHICK STANDARD; PRT; 1744 AA.
AC Q04205; Q91007; Q92011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
Tensin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=94350987; PubMed=8071358;
RA Lo S.H., An Q., Bao S., Wong W.K., Liu Y., Jamney P.A., Hartwig J.H.,
RA Chen L.B.;
RT "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA
RT sequence, expression, and characterization.";
RL J. Biol. Chem. 269:22310-22319(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95204530; PubMed=7896874;
RA Chuang J.Z., Lin D.C., Lin S.;
RT "Molecular cloning, expression, and mapping of the high affinity
RT actin-capping domain of chicken cardiac tensin.";
RL J. Cell Biol. 128:1095-1109(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen L.B.;
RL Submitted (XX-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1469-1744 FROM N.A.
RC TISSUE=Embryonic chondrocytes, and Embryonic heart;
RX MEDLINE=94039118; PubMed=8223621;
RA van de Werken R., Gennari M., Tavella S., Bet P., Molina F.,
RA Lin S., Cancedda R., Castagnola P.;
RT "Modulation of tensin and vimentin expression in chick embryo
RT developing cartilage and cultured differentiating chondrocytes.";
RL Eur. J. Biochem. 217:781-790(1993).
RN [5]
RP SH2 DOMAIN.
RX MEDLINE=91220073; PubMed=1708917;
RA Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,
RA Roberts T.M., An Q., Chen L.B.;
RT "Presence of an SH2 domain in the actin-binding protein tensin.";
RL Science 252:712-715(1991).
CC -!- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT
CC AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.
CC BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED
CC CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.
CC -!- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.
CC -!- TISSUE SPECIFICITY: HEART, GIZZARD, LUNG AND SKELETAL MUSCLE.
CC -!- PTM: TYROSINE-PHOSPHORYLATED.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC

CC or send an email to license@isb-sib.ch).

```
CC -----
DR EMBL; M96625; AAA59053.1; -
DR EMBL; L06662; AAA73949.1; ALT_INIT.
DR EMBL; Z18529; CAA79215.1; ALT_INIT.
DR EMBL; M74165; AAA49087.1; -
DR EMBL; X66286; CAA46992.1; -
DR PIR; A54970; A54970.
DR PIR; S27939; S27939.
DR HSSP; P16277; 1BLK.
DR InterPro; IPR006020; PTB PID.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
KW Actin-binding; Cytoskeleton; SH2 domain; Phosphorylation.
FT DOMAIN 66 342
FT 1472 1581
FT SH2.
FT C -> R (IN REF. 2).
FT CONFLICT 49 49
FT M -> T (IN REF. 2).
FT CONFLICT 61 61
FT Q -> PR (IN REF. 3).
FT CONFLICT 88 88
FT A -> T (IN REF. 2).
FT CONFLICT 404 404
FT T -> A (IN REF. 2).
FT CONFLICT 452 452
FT DV -> EL (IN REF. 2).
FT CONFLICT 508 509
FT A -> P (IN REF. 2).
FT CONFLICT 522 522
FT R -> A (IN REF. 2).
FT CONFLICT 664 664
FT P -> T (IN REF. 2).
FT CONFLICT 875 875
FT P -> A (IN REF. 2).
FT CONFLICT 909 909
FT MISSING (IN REF. 3).
FT CONFLICT 1102 1113
FT G -> A (IN REF. 2).
FT CONFLICT 1240 1240
FT E -> D (IN REF. 2).
FT CONFLICT 1480 1480
FT D -> E (IN REF. 2).
FT CONFLICT 1711 1711
FT SEQUENCE 1744 AA; 187214 MW; 5C3C8B6211935524 CRC64;
SQ
Query Match
Best Local Similarity 20.5%; Score 282; DB 1; Length 1744;
Matches 170; Conservative 94; Mismatches 255; Indels 320; Gaps 31;
QY 2 VTTPDPVSTSTSRWARDLOENPNRQPGPRVSEPHNSIVRIHIFTAIVSSNCRTE 61
DB 29 ITKQVDTDP-ATRS-----PRGQAH-----CKASRSMVTAAMESSC--- 65
QY 62 YQNIDLCAIYDRIIAIGYPATGTEANFNENKSVQTOQLTTRHGGKGVNKNLGGVY 121
DB 66 ----ELDLVIYIERIIAYSPTAEEQSPRNLREVAHMLKSKHG-DNVLFLNL-SERRH 119
QY 122 DADNFDGNYICPDMTDHPPPSLELNAFPCEAKLEADDKHVIACHKAGRGRTGVMT 181
DB 120 DISKLHPKVLDRGWPLDHTPALEKICSIKAMDWTLNAAAHNVVVLHNGKNGRLGVVA 179
QY 182 ALLIYNFPPSRQILDYYSIIRTKNKGVTI--PSQRYIYYVYHKLRR--ELNVLPLR 237
DB 180 AYMHYSNIGASADQALDRAMKRFYEDKVPVQPSQKRIIHYFSGLLSGSIKMNKPLF 239
QY 238 MQ-----LIGVYVERPPKWTGGGSKIKVEGVNGSTILFKPDPL---- 275
DB 240 LHHVIMHGIPNFKSGGCRPPFLKIYQAMQPVYTSGIYVNGDSQGTICITIFGLLLKGD 299
QY 276 IISKSNHQERATWLNMCNCTPNEFTDGEQKYGFGVSKRAYCFMVPEDAPVFVEGVDRI 335
DB 300 ILLKCVHKKFR-----SPTRDVI FRVQFH-----TCVAHDLDI-VFGKEDLDEAF 343
QY 336 REIGFLKFKSD-GKHGWFWNTWACDGGGLNGHGFYVDKTPYIGDDTSIGRKNGMRRN 394
DB 344 RD-----ERPFXGKVEFV-----FSY----- 360
QY 395 EITPMRKIDPTGNEFESPMQIVNPPGLEKHITEEQAMENYVGMIPPTYSKILHEKH 454
DB 361 -----GPEK-----IQGMEHLENGSPSVSDYNTSDPL----- 387
```

RESULT 5

```
AUX1_BOVIN
ID AUX1_BOVIN STANDARD; PRT; 910 AA.
AC Q27974;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Auxilin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=95220355; PubMed=7705342;
RA Schroeder S., Morris S.A., Knorr R., Plessmann U., Weber K.,
RA Vinh N.G., Ungewickell E.;
RT "Primary structure of the neuronal clathrin-associated protein
RL auxilin and its expression in bacteria.";
RL Eur. J. Biochem. 228:297-304(1995).
CC -!- FUNCTION: BINDS CLATHRIN HEAVY CHAIN AND PROMOTES ITS ASSEMBLY
CC INTO REGULAR CAGES.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- PTM: TARGET FOR COAT-ASSOCIATED CASEIN KINASE II IN VITRO.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09237; AAA79037.1; -
DR PIR; S68983; S68983.
DR InterPro; IPR001623; DnaJ N.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00226; DnaJ; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; UNKNOWN_1.
DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR PROSITE; PS50076; DNAJ_2; 1.
```

KW SH3-binding; Repeat; Phosphorylation.
 FT DOMAIN 33 44 3 X 4 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 33 36 1.
 FT REPEAT 37 40 2.
 FT REPEAT 41 44 3.
 FT SITE 60 344 TENSIN.
 FT SITE 406 414 SH3-BINDING (POTENTIAL).
 FT DOMAIN 463 757 PRO-RICH.
 FT DOMAIN 526 529 POLY-GLY.
 FT DOMAIN 846 910 J-DOMAIN.
 SQ SEQUENCE 910 AA; BC156DC1CF3487FD CRC64;

Query Match 4.2%; Score 217.5; DB 1; Length 910;
 Best Local Similarity 21.0%; Pred. No. 1.3e-05;
 Matches 211; Conservative 115; Mismatches 371; Indels 307; Gaps 52;

QY 60 TEYQNTDLCAVITDRIIAIGVPATGIEANFRNSKVTQOQFLTRRHGKGNVNFVNLGGY 119
 DB 54 TSYTKGDLDTVTSTRIIVMSPLDSVDIGFRNQVDDIRSLDSRH-LDHYTVYNLSPKS 112
 QY 120 YDADNFDGNVCFDMTHDHPHPSLEMAPFCREKEWLEADKHVAVHCKAGKGTGMV 179
 DB 113 YRTA-KFHSRVSECSWPIRQAPSLHNLFAVCNMYNLLQNPKNVCVHCLDGRAASSIL 171
 QY 180 ICALLIYINFY--PSRQILDYYSIIRTKNKGVTI--PSORRYIVYHYKL---RRELNY 233
 DB 172 VGAMFIFCNLYSTPGAVRLLY-----AKRPGIGLSPSHRRYLVGMCDLLADKPYRPHF 225
 QY 234 LPLRMQLIGVYVERPPKWTGGGSKIKVEVNGSTILFKPDPLIISKNNHQRERATWLNC 293
 DB 226 KPLTKISIV-----SPVPFF-----NKQR-----NGC 248
 QY 294 DTNEPDTGEQKH-----GFVSKRAYCFMVPEADPVF-----VEGDVRIIDIREI----- 338
 DB 249 RPYCDVLIGETKIYITTCADFERMKEYRV---QDGKIFPLSITVQGDVVVSWYHLRSTIG 305
 QY 339 -GFLKFSOGKIGHWFTNMF-----ACDGLNGHGFYVDKTPYIGD 381
 DB 306 SRLQAVTNTQIFQHFHGFIPLDITVLKFTKPELDACD-----VPEKYPQLFQ 355
 QY 382 DTSIGRKNRMARNETPMRKIDPETGNEPESPMQ-----IVNPPGLEKHTTEQAMENYTN 436
 DB 356 VT-----LDVELQPHDKV-----MELTPPEHYCTKDVPNSILFSSHQEQ--DTLVL 401
 QY 437 YGMIP-----PRY-----TISKIL--HEKHEKGIKDDY-----NDRKLPMGDKSYTES 478
 DB 402 GGQAPIDIPDPNPRHFGQGGFTSTLCWQDQKSEKCEEDHAALVNQSEQSDDELLTSL 461
 QY 479 GKSGDIRGVGGPEIPY-----KAEHVLTFFPVYEMD-----RALKSKDLNNGMKLHV 526
 DB 462 SPHGNANG-----DKPHAARKSKKQPEAPAPPPEDVDLLGLEGSVSKNFSS----- 510
 QY 527 VLRCVDTROSKWMEKSEVFG-----NLAFF-----NEST-RLQALQTM 564
 DB 511 --PAAPPSNELL--SDLFGGGAAGPVQSGQVDDVDFHPSGPTSTQSTPRSATSISA 566
 QY 565 NPKWR--PEPCAFSGKAEMHYPPSVRYNSND--GKYNAGCSNLSVDFEHRNIAVLNRY 621
 DB 567 SPTLRVGEATDPFGA-----PS-KPSGQDLGLSPLNTASAS--SDPF----- 607
 QY 622 CRYFYKQSTSRSPRYKRCYPLIKKHFIYIPADTDDVDENGOPFHS--PEHYIKEQEKI 680
 DB 608 ----LQTRSPSPVTHASS-----TPAVNIQPDVSGAWDHTTKPGGF----- 645
 QY 681 DAEEAKAGTENTGPTSGSS-----APGTIKK-----TEASQSKVKPATEDEL--- 724
 DB 646 ----GWGSKSAATSTGSSHGTPHONKPTQLDPADLGTGLGSSFAKSPSTPTCLGG 700
 QY 725 -PPARLPDNRFPVVG-----VDFENPEESCEHKTVESTAGPELHFLPHESY 773
 DB 701 FPLSPSPKASQPMGGGQWQGGYNNQOTQSKPQSSMPHSSPQNRPN-----YVNSF 753
 QY 774 HNTAGNMLRDYHTDSEVKIAEOEAKAFVDQLLNGQVLQBFMKQPKVPSDNSADYVT 833

DB 754 SSMPGGQNERGKAAANLEK---QXADFED-LISQGG-----FNAHKDK----- 794
 QY 834 GOAEVFKAQIALLEQSEDFQRVQANAEVDLEHTLGEAFERFGHVHVESNSSKNPKALK 893
 DB 795 -----KGPRTIAE-----MRKEEMAKEMDPEKL-----KILEWIEGKERNIRALL 834
 QY 894 TREQMVKETGDKTQKTRNHVLLHLEANHRVQIERRETCPHELHPE 937
 DB 835 STMHTVLWAGETKWKPVG--MADLVTPQVQVKYRKAVLVVHPD 876

RESULT 6
 GAK_RAT ID GAK_RAT STANDARD; PRT; 1305 AA.
 AC P97874;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cyclin G-associated kinase (EC 2.7.1.-).
 GN GAK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97165969; PubMed=9013862;
 RA Kanaoka Y., Kimura S.H., Okazaki I., Ikeda M., Nojima H.;
 RT "GAK: a cyclin G associated kinase contains a tensin/auxilin-like domain.";
 RT FEBS Lett. 402:73-80(1997).
 RL
 CC -!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an auxilin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression oscillates slightly during the cell cycle, peaking at G1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the trans-Golgi network. Also seen on the plasma membrane, probably at focal adhesions (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: Contains 1 tensin domain.
 CC -!- SIMILARITY: Contains 1 J domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).
 CC EMBL; D38560; BAA18911.1; -.
 DR PIR; T31096; T31096. DnaJ_N.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00226; DnaJ_1; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00271; DnaJ_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Nuclear protein; Endoplasmic reticulum; Cell cycle.
 FT DOMAIN 40 315 PROTEIN KINASE.
 FT ACT SITE 173 173 BY SIMILARITY.
 FT DOMAIN 405 689 TENSIN.
 FT DOMAIN 1241 1305 J-DOMAIN.

DR	InterPro; IPR000387; TYR_phosphatase.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW	Hypothetical protein: Hydrolase
SEQUENCE	434 AA; 50152 MW; E56739475D1FA898 CRC64;
Query Match	4.1%; Score 209.5; DB 1; Length 434;
Best Local Similarity	23.8%; Pred. No. 1.4e-05;
Matches	91; Conservative 44; Mismatches 146; Indels 101; Gaps 15;
QY	67 LDCAYITDRIIAIGYPA-TGIEANFNRSKVQTOQFLTRRHGKGNVKVFNLRG-----GYYY 121
DB	42 LDISYILVNLI VCSYPVNTYPKLLYRNSLDLFLFTLVYHGKGNFRIFNFRGKEKSDYK 101
QY	122 DAD-----NFD-----GNVIC--PDMTD 137
DB	102 DNDLIGIAAKFSKDFEIQELRSTLINDGKIPISPIDLRETRTLVEBETNNVICERIGWLD 161
QY	138 HPPSLLELMAPPFCEAKLEWLEADDDKHVIAVHCAGKGRGTGVMICALLI-YINFYSPSPQI 190
DB	162 HPPPPPELLEEIVDGIENLYLSYKRVAVLHCRMGKGRSGMITVAVLMKYLQCPLEEARL 221
QY	197 LDYYSIIRTKNNKGVITIPQRRYIYY-----HKLRERELNYLPLRMQLIGVVVERPPKT 251
DB	222 IFQARFKYGMTNGVTIPSQLRYLRYHEFFITHEKAAQE-----GISNE----- 265
QY	252 WGGGSKI KVEVNGSGTILFKPPLIISKNHQERATWLNNCPTPNEFDTEQKYHGFFVS 311
DB	266 ---AVKFKFKRLAKMTFURPSSLITSESAIVTTKIQHVN--DNRNALLTRKVVYSDIMA 320
QY	312 KRA---YCFMVPEDAPFVVEGVDVIRDIRIGFLKFSDGKI-----GHVWFNTMFACDG 362
DB	321 HECGGNMTIFGRDY-LTLENDCRIEF-TLGTSSKKAASSIIISWTSCASCLNLI----- 372
QY	363 GLNGGHFEYVDKTPQYIGDDTS 384
DB	373 -----YLETIMHIKKDSS 386
RESULT 8	
GAK_HUMAN	
ID	GAK_HUMAN STANDARD; PRT; 1311 AA.
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Cyclin G-associated Kinase (EC 2.7.1.-).
GN	GAK.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP	TISSUE=Fibroblast;
RC	MEDLINE=97446136; PubMed=9299234;
RC	Kimura S.H., Tsuruga H., Yabuta N., Endo Y., Nojima H.;
RT	"Structure, expression, and chromosomal localization of human GAK.";
RL	Genomics 44:179-187(1997).
RN	[2]
RN	SEQUENCE OF 981-1311 FROM N.A.
RP	TISSUE=Placenta;
RC	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worlev K.C., Hale S., Garcia A.M., Gav L.J., Hulvik S.W.,


```
CC spindle pole body through to late anaphase.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY, CDC14 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: AL158056; CAB76271.1; -
CC PIR: T50099; T50099.
CC HSP: P29350; 1GWZ.
CC GenesDB SPombe; SPAC1782.09c; -
CC InterPro; IPR000340; DS phosphatase.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF00782; DSPC; 1.
CC PRINTS; PR00700; TRYPPHPTASE.
CC PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
CC PROSITE; PS00566; TYR PHOSPHATASE 2; 1.
CC Hydrolase; Cell cycle; Mitosis; Septation; Nuclear protein;
KW Phosphorylation.
FT ACT_SITE 286 286 BY SIMILARITY.
SQ SEQUENCE 537 AA; 60253 MW; F5B50A8C0924C7EA CRC64;

Query Match 2.7%; Score 141; DB 1; Length 537;
Best Local Similarity 24.6%; Pred. No. 0.26; Indels 82; Gaps 16;
Matches 70; Conservative 47; Mismatches 85;

QY 37 YHNSIVERIRHIFRTAVSSNRCRTBYONIDL-----DCAYITDRIIAIGYPAT 84
D 142 YVITIDOCVGLWRARESS--ILNIRNIDVDHYETVERVENDFNWISPFIAFASP-- 196
QY 85 GLEANFRNSKVOTQ-----FLTRHGKGNVKNVFNLRGGYYDANFDGNV--- 130
D 197 -IQAGNWAHSTRPKKLPQFAIVLDFYVANK-----VKLIVRLNGLYDKKTFE-NVGIR 249
QY 131 ---ICFDMTDHHPSPLELMAPFCREAKWL-----EADDKHVTAVHCKAGKGTGMICAL 183
D 250 HKEMVFE--DGVTPELSLV-----KEFIDTVEEEDGVIAVHCKAGLGRGTCLIGAY 300
QY 184 LIYINFPSPROILDYGIIRTKNNKVTIPSQRYI-----YYHKLRLERELNVL 234
D 301 LIYKCF-TANEVIAVMRMR-----PGMVVGQQHMLHINQVHFRAFYERKAMGAIQQA 355
QY 235 PLRMOLIGYVERPPK-----TWGGGSKIKVEVNGSTILFKPDP 274
D 356 TAAEPL-----ATPPRPLNATNGTSQ-----SNISTPLPEPTP 389

RESULT 10
GIAN HUMAN
ID GIAN HUMAN STANDARD; PRT; 3259 AA.
AC Q14789; Q14398;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Golgi autoantigen, golgin subfamily B member 1 (Giantin) (Macroglolin)
DE (Golgi complex-associated protein, 372-kDa) (GCP372).
DE GOLGB1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187728; PubMed=7511208;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RA "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
```

```
RT protein (giantin).";
RL Mol. Cell. Biol. 14:2564-2576 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257116; PubMed=8198703;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RT "Macroglolin -- a new 376 kD Golgi complex outer membrane protein as
RT target of antibodies in patients with rheumatic diseases and HIV
RT infections.";
RL J. Autoimmun. 7:67-91 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95100974; PubMed=7802676;
RA Sohma M., Misumi Y., Fujiwara T., Nishioka M., Ikehara Y.;
RT "Molecular cloning and sequence analysis of a human 372-kDa protein
RT localized in the Golgi complex.";
RL Biochem. Biophys. Res. Commun. 205:1399-1408 (1994).
CC -!- FUNCTION: May participate in forming intercisternal cross-bridges
CC of the Golgi complex.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Membrane-associated protein, Golgi.
CC -!- DISEASE: Antigen in chronic rheumatoid arthritis and in the
CC autoimmune disease Sjogren's syndrome.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: X75304; CAA53052.1; -
CC EMBL: D25542; BAA05025.1; -
CC PIR: A56539; A56539.
CC PIR: I52300; I52300.
CC Genes; HGNC:4429; GOLGB1.
CC MIN; 602500; -
CC GO; GO:0000139; C:Golgi membrane; TAS.
CC GO; GO:0005795; C:Golgi stack; TAS.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0007030; P:Golgi organization and biogenesis; TAS.
KW Golgi stack; Antigen; Coiled coil; Transmembrane.
FT DOMAIN 1 3235
FT TRANSMEM 3236 3256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 3257 3259 LUMENAL (POTENTIAL).
FT DOMAIN 48 593 COILED COIL (POTENTIAL).
FT DOMAIN 677 1028 COILED COIL (POTENTIAL).
FT DOMAIN 1062 1245 COILED COIL (POTENTIAL).
FT DOMAIN 1301 1779 COILED COIL (POTENTIAL).
FT DOMAIN 1828 3185 COILED COIL (POTENTIAL).
FT DOMAIN 2420 2423 POLY-GLU.
FT DOMAIN 2993 2996 POLY-SER.
FT CONFLICT 1 39 MISSING (IN REF. 3).
FT CONFLICT 215 215 A -> AOLSSM (IN REF. 3).
FT CONFLICT 1765 1765 D -> G (IN REF. 3).
FT CONFLICT 2950 2950 H -> D (IN REF. 3).
SQ SEQUENCE 3259 AA; 376075 MW; 60376A20D8A178DD CRC64;

Query Match 2.7%; Score 138.5; DB 1; Length 3259;
Best Local Similarity 21.7%; Pred. No. 4.6;
Matches 97; Conservative 67; Mismatches 163; Indels 121; Gaps 22;

QY 525 HVVLRCDVTRDSKMKSEVFGNL-----AFINSTRRL-----QALTONPKWRPEPCAFG 576
D 1634 HVV-----EAVRQEKQLYKLRSTEANKKETKQLQEAQEEMEKMKRFAKSKQ 1686
QY 577 SKGAEMHYPPSVRYSSND-----GKYNAGCSENLVDSFFEHRLAVLNRYCRYK 627
D 1687 QKILELE-----EENDRLAEVHPADGTAKECNLTLS----- 1719
QY 628 QRSTSRSRYPK-KFRYCPLIKKHFYIPADTDDVDENGQFFPHSPHYIKOEKIDAEKAA 686
```

DB 1720 SNASMKELERVMYETLSKQFSLMSKDSLSSEVQDLKQKQIEDNVSKQANLEATE-- 1777
 QY 687 KGIENTGPSTGS-SAPGTIKKTEASQSDKVPKATEDELPPARLPDNRVFPVGVDFEN 745
 DB 1778 KHDNQTNVTEGTQSPGETEQD-SLSMSTRPTCSSEVPSAKSAN-----PAVSKDFSS 1831
 QY 746 PREESCEHKTIV-----ESIAGFPELHLPFHESYH--PNTAGNMLRQDYHTDSVKIAEQEA 799
 DB 1832 HDEINNYLQOIDQLKRIAGLEERKQKNEFQSTLENEKNLTLLSQISTKDGELKMLQBEV 1891
 QY 800 KAFVDOLLNGQGVLOEFMKQFVPS-----DNSPADVVTGQAEVF 839
 DB 1892 TKM--NLIN-QIQBELSRVTKLKTABEEKDDBERLMNQALNGSIGNYC---QDVT 1945
 QY 840 KAOI--ALLEQ-----SE-DFORVQANAEVDLEHTLGEAFERFGHVVEESNGSK 887
 DB 1946 DAQIKNELLESEMKLKKCVSELEBEKQLVKTEKVESEIRKEY-----LEKIQGAQK 1999
 QY 888 NP-----KALKTRQOMVKTGKD 905
 DB 2000 EPGNKSHAKELOELLKQEVKQLOKD 2027

RESULT 11

SPS_SOLTU
 ID SPS_SOLTU STANDARD; PRT; 1053 AA.
 AC Q43845;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
 phosphate glucosyltransferase).
 GN SPS.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Desiree; TISSUE=Leaf;
 RX MEDLINE=95201832; PubMed=7894514;
 RA Zremer R., Salanoubat M., Willmitzer L., Sonnewald U.:
 RT "Evidence of the crucial role of sucrose synthase for sink strength
 RT using transgenic potato plants (Solanum tuberosum L.).";
 RL Plant J. 7:97-107(1995).
 CC -!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
 CC THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
 CC THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
 CC PHOTOASSIMILATES OUT OF THE LEAF.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
 CC sucrose 6-phosphate.
 CC -!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
 CC MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
 CC -!- PATHWAY: Sucrose synthesis.
 CC -!- SUBUNIT: Homodimer or homotetramer (By similarity).
 CC -!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
 CC ENZYME FUNCTION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X73477; CAA51872.1; --
 DR FIR; S34172; S34172.
 DR InterPro; IPR001296; Glyco trans 1.
 DR Pfam; PF00634; Glycos_transf_1; 1.

KW Transferase; Glycosyltransferase; Phosphorylation.
 SQ SEQUENCE 1053 AA; 118292 MW; D6C933798567B20A CRC64;
 Query Match 2.6%; Score 136; DB 1; Length 1053;
 Best Local Similarity 18.7%; Pred. No. 1.4;
 Matches 154; Conservative 112; Mismatches 283; Indels 276; Gaps 41;
 QY 196 ILDYYSIIRTKN---NKGVTIPSQRRYYVYHKLREELNLP--LRMLQIGVVVERPPK 250
 DB 170 LISLHGLIRGENMELGRSDSDTGQVQYVVEL-----ARALGSMGPVYRVDLITRQVSSPEV 225
 QY 251 TWGGGSK-----IKVEVGNGS-----TILFKPDPLIISKSNHOREATWLNNDT 295
 DB 226 DWSGEPTLAPLSTDGLMTGESSGAYIIRIFGP-----REK----- 265
 QY 296 PNEFDTGQKHGFVSKRAYCFMVPEDAPVVEGVDRIREIGFLKFKSGCKIGH--V 352
 DB 266 -----YIPKEQLWPYIPE-----FVDGALAHIIQ-----MSKVLGEQIGSGYVP 304
 QY 353 W-----FNTMFACDGLN-----GGHPEYVDKTPYIGDDTSIGRKNMRRNET 396
 DB 305 WPAIHGHYADGDSALLSGALNVPMFTGHSIGRDKLEQLAQ-----GRKSDKEINST 360
 QY 397 --PMRKIDPE-----TGNEPESWQIVN--PPGLEKHITBEQAMENYNTYGM 439
 DB 361 YKIMRIEAEELTLDASEIVITSTQEIDEQWRLYDGFDPILERKL-RARIKENVSCYGR 419
 QY 440 IPPRYTISKILHEKHEKGIKVDYNDKRLPMGDKSYTESGKGD-----IRGVGP-- 490
 DB 420 FMPRAVIPPQMGFEFHHIVPHEGDM-----GETEGSEDGKTDPDPIWAEIMRPFSPNRK 473
 QY 491 ---FEIPYKAEHVLTTPVYENDRALKSKDLNMGKMLHVLCVDTTRS----- 536
 DB 474 PMILALAPDPDKNLTLLVKAPGECRPLRDAN---LTLMNGNRDNIDEMSTNSALLS 530
 QY 537 --KXMEKESEVGNLAF--HNES-----TRRLQALTO---MNPKW-RP-----EPCAFG- 576
 DB 531 ILKMDIKDLYGVQAVPKHKQSDVPDIYRLAAKTGVFINPAFIEPGLTLIEAAAYGL 590
 QY 577 -----SKGAEMHYPPSVRYSSNDGKYNACSENLVSDFFEH-----RNI 615
 DB 591 PMVATKNGG---PVDIHRVLDNGLLVDPHQDQAADALLKLKLVADKQWAKCRANGLKNI 646
 QY 616 AVLN--RVCYFYKORSTSRSPRYKPCPLIKGHFVIPADTDVDSNGQPFHFSPEHY 673
 DB 647 HLFWSPEHCKTSLRSIASCPRQPRWLR-----SIDDDDENSET--DSPSDS 691
 QY 674 IKE-----QEKIDAEAKAGIENTGPTSGSSAPGTIKKTEA 710
 DB 692 LRDIHDIISLNRFSLDGKDNKENADNTLDPEVRRSKLENAVLSL---KGALKSTSK 747
 QY 711 S-QSDKVKPATEDELPPARLPDNRV---FPVGVGD-----FENPEERCE 752
 DB 748 SWSDDKA-----DQNPAGAKFPARRRRRHIFVIAVDCCDASSGLSGSVKKIFEAVEKERAE 802
 QY 753 H-----KTVESIAGFEPLHLFHSYHPNTAGNMLRQDYHTDSVKIAEQEAK 800
 DB 803 GSIGFILATSNISEVQSFLISEGNMPTDFDAYICNSGDLIYSSFHSEQNPFFVVDLYH 862
 QY 801 AFVDOLLNGQGVLOEFMK-----QFKVPSDNPADY 831
 DB 863 SHIEYRWGGEGLRKLTLVWAASIIDKNGENGHDHIVVEDEDNSADY 907
 ID UN89 CAEEL STANDARD; PRT; 6632 AA.
 AC Q01761; Q17362;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
 GN UNC-89 OR C09D1.1.


```

Db      3922  FLPQVKAIVVTGETA-----VLEGKISKPRSPKVKWYKNGBELKPSDRVKINLDDGTQ 3970
QY      735  RFPVWGVDPENPEESCEHK-----TVESIAGFPEPLEHLEFHESYHENTAGNML 782
Db      3977  RLTVTNAKLDDMDVEYRCEASNEFGDWSVDLTLTVKEPAQVAP-----GFFKELSAIQV 4029
QY      783  RQDYHTDSEVKIA--BOEAKAFVDQL-----LNGQGVLOQEFMKQFKVPSNSFA 829
Db      4030  KETETAKFECKVSGTKPDPVKWFKDGTPLKEDKRVHPFESDDGTQRLVIEDSKTDDQGNVR 4089
QY      830  DYTGTGAQVFKAQIALLEQSEDQFQVQANAEVDLEHTLTGEAFERFGHVVEESNGSSKNP 889
Db      4090  IEVNSDAGVANSKPLTVVPVSETLTKIKGLTDVNV--TQTKI-----LLSVEVEGPKTV 4143
QY      890  KALKTREQMV-KETGDKDTOKTRNHVLLHLEANHRVQIERRE 929
Db      4144  KWTGKTETVSSQTTKIVQT-----ESEKLEISAE 4176

RESULT 13
YLPK CAEEL
ID_YLPK CAEEL STANDARD; PRT; 264 AA.
AC P91301;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.3 kDa protein F46F11.3 in chromosome I.
GN F46F11.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 tensin domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U88173; AAK21381.1; -.
DR PIR; T25762; T25762.
DR WormPep; F46F11.3; CEI0600.
KW Hypothetical protein.
FT DOMAIN 31 264 TENSIN.
SQ SEQUENCE 264 AA; 30300 MW; 3DF3698F292BCSE5 CRC64;

Query Match 2.6%; Score 133; DB 1; Length 264;
Best Local Similarity 21.1%; Pred. No. 0.3;
Matches 40; Conservative 42; Mismatches 90; Indels 18; Gaps 6;

QY 41 IVERIRHIFRTAVSSNRCTEYQNIOLDCAYITDRIIATGYPATGLEANFRNSKVOTQOF 100
Db 15 LVEKLAR-----KQMKDKRKEGVQVE--YITSLRILVLSCTSETSERKFVESLLKASQ 65
QY 101 LTRHRCKGNVKNVFNLRGGYYVDADNFDGNVICFDMTDHPPSLMELMAFFCREAKWEAD 160
Db 66 IQNAHNK-HIRVWNVNSQRHDISSSLD--AIPGWPSETAPSLKELCTTCKNLQDWMLEH 122
QY 161 DKHVIHVHCKAGKRGRTGVMTCALLIYINFPSPRQLIDYYSIRTKNN-----KGVTPSQ 216
Db 123 PLNIAVIFCKGGLERCAIVVNAFMRENAISATDSDVDREFSMQRFSEFLGPDGP--PSY 180
QY 217 RRVYYVYHKL 226
Db 181 KRYLGYFSSL 190

```

```

#####
926 DAGESEKRCVPPSSNFTDYMCDWDCSIIYVASSPSHVLKHLSEHVABELRLLCRWGCA 989
#####

933 ELHPEDKIPRIAHSENSFSDSNFDQA 959
#####

986 DPTFRNRWSLTHIQDGHCHNEAQLKAA 1012
#####

RESULT 15
ANK2 HUMAN
ID ANK2 HUMAN STANDARD; PRT; 3924 AA.
AC Q01484;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RP TISSUE=Brain stem;
RC MEDLINE=91302466; PubMed=1830053;
RX Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RN J. Cell Biol. 114:241-253(1991).
RN [2]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Brain stem;
RC MEDLINE=94075409; PubMed=8253844;
RX Chan W., Kordeli E., Bennett V.;
RA "440-kD ankyrinB: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RN J. Cell Biol. 123:1463-1473(1993).
RN [4]
SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tee W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q01484-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC Name=3;
CC IsoId=Q01484-3; Sequence=VSP_000268;
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: Contains 23 ANK repeats.
CC -1- SIMILARITY: Contains 1 Death domain.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
for details)

```


Fri Dec 13:18:53 2003

Db 2123 SEETEKAQLHLDQVL 2137

Search completed: December 10, 2003, 20:32:53
Job time : 20.6821 secs

us-09-205 a-310.rsp

Page 15

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:29:32 ; Search time 54.8125 Seconds
(without alignments)
4529.010 Million cell updates/sec

Title: US-09-205-658A-310
Perfect score: 5168
Sequence: 1 NVTPTDVPSTSTRMARDL.....IAHFSNSFSDSNFDQAIYL 962

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mnc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5168	100.0	962	5	044405 caenorhabdi
2	505.5	9.8	412	13	Q90XY3
3	491.5	9.5	403	11	Q54857
4	474.5	9.2	403	4	O43460
5	460.5	8.9	338	4	O14781
6	459.5	8.9	402	13	Q9PUT6
7	442	8.6	509	5	Q9V3L4
8	442	8.6	514	5	Q9V413
9	441.5	8.5	506	5	Q9U470
10	441.5	8.5	511	5	Q9Y0B5
11	438	8.5	632	10	Q8H106
12	437	8.5	628	10	Q9SN07
13	435	8.4	418	5	Q9Y0B6
14	431	8.3	515	5	Q8T658
15	431	8.3	533	5	Q8T9S7
16	403.5	7.8	412	10	Q9FLZ5

17	401.5	7.8	611	10	Q9LT75	Q9LT75 arabidopsis
18	401.5	7.8	611	10	Q8GZT8	Q8GZT8 arabidopsis
19	400.5	7.7	369	4	Q8IVA5	Q8IVA5 homo sapien
20	368	7.1	445	4	Q8WML5	Q8WML5 homo sapien
21	348.5	6.7	326	4	Q8WML4	Q8WML4 homo sapien
22	342	6.6	645	11	Q91X02	Q91X02 mus musculus
23	342	6.6	664	11	Q91X03	Q91X03 mus musculus
24	338.5	6.5	591	11	Q91X01	Q91X01 mus musculus
25	333.5	6.5	533	4	Q8NCS8	Q8NCS8 homo sapien
26	315.5	6.1	1735	4	Q9HBL0	Q9HBL0 homo sapien
27	301	5.8	1715	6	Q9GLM4	Q9GLM4 bos taurus
28	273	5.3	222	11	Q8C6V6	Q8C6V6 mus musculus
29	270	5.2	624	11	Q8BUA7	Q8BUA7 mus musculus
30	261	5.1	398	4	Q9NV48	Q9NV48 homo sapien
31	259.5	5.0	1445	4	Q8IZW7	Q8IZW7 homo sapien
32	247.5	4.8	348	3	O94526	O94526 schizosacch
33	244	4.7	280	11	Q8BSR7	Q8BSR7 mus musculus
34	240.5	4.7	391	4	Q8NAD0	Q8NAD0 homo sapien
35	220.5	4.3	913	4	O75061	O75061 homo sapien
36	214	4.1	1381	11	Q8CJ95	Q8CJ95 mus musculus
37	214	4.1	1400	11	Q8CGB6	Q8CGB6 mus musculus
38	213	4.1	1409	4	Q8NFF9	Q8NFF9 homo sapien
39	213	4.1	1419	4	Q8NFG0	Q8NFG0 homo sapien
40	210	4.1	1285	4	Q9UPS7	Q9UPS7 homo sapien
41	176.5	3.4	885	11	Q8BM74	Q8BM74 mus musculus
42	162	3.1	1271	5	Q25860	Q25860 plasmodium
43	154	3.0	446	5	Q9UAX0	Q9UAX0 caenorhabdi
44	154	3.0	1233	5	Q8IJ56	Q8IJ56 plasmodium
45	153.5	3.0	913	4	Q9HCH5	Q9HCH5 homo sapien

ALIGNMENTS

RESULT 1

ID	O44405	PRELIMINARY;	PRT;	962 AA.
AC	O44405; Q9TVU8;			
DT	01-JUN-1998 (TREMREL. 06, Created)			
DT	01-JUN-2001 (TREMREL. 17, Last sequence update)			
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)			
DE	T07A9.6 protein (DAF-18 protein).			
GN	T07A9.6 OR DAF-18.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	None;			
RT	"Genome sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium.";			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Scheet P., Maggi L.;			
RT	"The sequence of C. elegans cosmid T07A9.";			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Waterston R.;			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rouault J.P., Kuwabara P.E., Sinilnikova O., Duret L.,			
RA	Thierry-Mieg D., Billard M.;			
RT	"Regulation of dauer larva development by the tumor suppressor PTEN			
RT	homologue daf-18 in Caenorhabditis elegans.";			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			

RN RP SEQUENCE FROM N.A.
 RX MEDLINE=99102962; PubMed=9885576;
 RA Ogg S., Ruvkun G.;
 RT "The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like
 RT metabolic signaling pathway";
 RL Mol. Cell 2:887-893(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99178991; PubMed=10077613;
 RA Gil E.B., Malone Link E., Liu L.X., Johnson C.D., Lees J.A.;
 RT "Regulation of the insulin-like developmental pathway of
 RT Caenorhabditis elegans by a homolog of the PTEN tumor suppressor
 RT gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2925-2930(1999).
 DR EMBL; AF036706; AAK39284.1; -;
 DR EMBL; AJ131181; CAA10315.1; -;
 DR EMBL; AF098286; AAD03420.1; -;
 DR EMBL; AF126286; AAD21620.1; -;
 DR WormPep; T07A9.6; CE26385
 DR InterPro; IPR000387; TYR_phosphatase.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 962 AA; 110328 MW; 79212EF05C959837 CRC64;

 Query Match 100.0%; Score 5168; DB 5; Length 962;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MVTTPDPVSTSTRSMARDLQENPNRQGEPRVSEPYHNSIVERIRHIFRTAVSSNRCT 60
 DB 1 MVTTPDPVSTSTRSMARDLQENPNRQGEPRVSEPYHNSIVERIRHIFRTAVSSNRCT 60

 QY 61 EYQNDLDCAYITDRIIAIGPATGIEANFRNSKVOTQFLTRRHGKGNVFNLRGGY 120
 DB 61 EYQNDLDCAYITDRIIAIGPATGIEANFRNSKVOTQFLTRRHGKGNVFNLRGGY 120

 QY 121 YDADNPDGNCVCFDMDTHPPSLLEMAPFCRAKEWLEADKHVIAVHCAGKGRGTGVI 180
 DB 121 YDADNPDGNCVCFDMDTHPPSLLEMAPFCRAKEWLEADKHVIAVHCAGKGRGTGVI 180

 QY 181 CALLIYINFPSPQRLDYSIIRTKNNKGVITPSORRYIYYHKLRLRELNYLPLRMOL 240
 DB 181 CALLIYINFPSPQRLDYSIIRTKNNKGVITPSORRYIYYHKLRLRELNYLPLRMOL 240

 QY 241 IGVYVERPKTWGGGSKIKEVGVNGSTILFKPDPLIISKSNHQRERATWLNCCDTPNEFD 300
 DB 241 IGVYVERPKTWGGGSKIKEVGVNGSTILFKPDPLIISKSNHQRERATWLNCCDTPNEFD 300

 QY 301 TGEQKTHGVSKRAYCFMVPEDAPVPEGDVDRIDREIGFLKKPSDGKIGHVWFTMTFAC 360
 DB 301 TGEQKTHGVSKRAYCFMVPEDAPVPEGDVDRIDREIGFLKKPSDGKIGHVWFTMTFAC 360

 QY 361 DGLNGGHPEYVDKTPYIGDDTISGRKNGMRNETPMKIDPETGNEPESPMQIVNPPG 420
 DB 361 DGLNGGHPEYVDKTPYIGDDTISGRKNGMRNETPMKIDPETGNEPESPMQIVNPPG 420

 QY 421 LEKHITTEQAMENYNYGMIPRYTISKILHEKHEKGIKVDYNDKRLPMGDKSYTESGK 480
 DB 421 LEKHITTEQAMENYNYGMIPRYTISKILHEKHEKGIKVDYNDKRLPMGDKSYTESGK 480

 QY 481 SGDIRGVGPFPIPKAEHVLTFPVYENDRALKSKDLNNGMKLHVLLVCVDTROSKME 540
 DB 481 SGDIRGVGPFPIPKAEHVLTFPVYENDRALKSKDLNNGMKLHVLLVCVDTROSKME 540

 QY 541 KSEVFGNLAFHNESTRRLQALQTMNPKWRPECAFGSKGAEMHYPPSVSYSSNDGKYNGA 600
 DB 541 KSEVFGNLAFHNESTRRLQALQTMNPKWRPECAFGSKGAEMHYPPSVSYSSNDGKYNGA 600

 QY 601 CSENLSVDFEHRNIAVLNRYCRYFYKQSTSRSPRYKFRYCPLIKGHFYIPADTDDVD 660
 DB 601 CSENLSVDFEHRNIAVLNRYCRYFYKQSTSRSPRYKFRYCPLIKGHFYIPADTDDVD 660

QY 661 ENGQPFPHSPHYIKEQEKIDAEKAAKGIENTGPSTSGSSAPGTIKKTEASQSDVKVPAT 720
 DB 661 ENGQPFPHSPHYIKEQEKIDAEKAAKGIENTGPSTSGSSAPGTIKKTEASQSDVKVPAT 720

 QY 721 EDELPPARLPDNNRRFPVGVDFENPEESCEHKTVESIAGPEPLEHLFHESYHNTAGN 780
 DB 721 EDELPPARLPDNNRRFPVGVDFENPEESCEHKTVESIAGPEPLEHLFHESYHNTAGN 780

 QY 781 MLRDYHTDSEVKIAEQEAKAFVQDQLNGQGVQLQFMKQFVPSDNSFADYVVGQAEVFK 840
 DB 781 MLRDYHTDSEVKIAEQEAKAFVQDQLNGQGVQLQFMKQFVPSDNSFADYVVGQAEVFK 840

 QY 841 AQIALLEQSEDQFQVQANAEVDLEHTLGEAFERFGHVVEESNGSKPKALKKTREOMVK 900
 DB 841 AQIALLEQSEDQFQVQANAEVDLEHTLGEAFERFGHVVEESNGSKPKALKKTREOMVK 900

 QY 901 ETGKDTQKTRNHVLLHLEANHRVQIERRCTPELHPEDKIPRIAHFSENSFSDSNFDOAI 960
 DB 901 ETGKDTQKTRNHVLLHLEANHRVQIERRCTPELHPEDKIPRIAHFSENSFSDSNFDOAI 960

 QY 961 YL 962
 DB 961 YL 962

 RESULT 2
 Q90XY3
 ID Q90XY3 PRELIMINARY; PRT; 412 AA.
 AC Q90XY3;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE PTEN.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21455682; PubMed=11571655;
 RA Yu W.P., Fallen C.J., Tay A., Jirik F.R., Brenner S., Tan Y.H.,
 RA Venkatesh B.;
 RT "Conserved synteny between the Fugu and human PTEN locus and the
 RT evolutionary conservation of vertebrate PTEN function";
 RL Oncogene 20:5554-5561(2001).
 DR EMBL; AF325922; AAL08419.1; -;
 DR InterPro; IPR000387; TYR_phosphatase.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 412 AA; 47974 MW; 8ABEBD8B71346CE3 CRC64;

Query Match 9.8%; Score 505.5; DB 13; Length 412;
 Best Local Similarity 35.7%; Pred. No. 4.1e-27;
 Matches 115; Conservative 48; Mismatches 102; Indels 57; Gaps 9;

 QY 48 IFRTAVSNCRCTEYQNDLDCAYITDRIIAIGPATGIEANFRNSKVOTQFLTRRHGK 107
 DB 4 IIKENVSNRKRYQEDGDFDLTYIPNLIAMGPAERLEGVYRNNDVVRFLDSKH-K 62

 QY 108 GNVKFNLRGGYVYDADNFDGNVICFMDTHPPSLLEMAPFCRAKEWLEADKHVIAV 167
 DB 63 NHYKIYNLCARHYDAKFNCRVAQYPPEDHNPQLEIKPFCELDQWLSDDNHAAI 122

 QY 168 HCKAGKGTGVMICALLIYINFPSPROILDYYSIIRTKNNKGVITPSORRYIYYHKL 227
 DB 123 HCKAGKGTGVMICALLIYINFPSPROILDYYSIIRTKNNKGVITPSORRYIYYHKL 182

 QY 228 ERELNYLPLRMOLIGVYVERPKTWGGG-----KIKVEGNGSTILFKPDPLIIS 278

```
Db 183 KQLEYKPVALLFKHMFETLPMFSGGTGTCNPQPVVYQLKVKIHTSNPS----- 230
Qy 279 KSNHQRERATWLNCDTNEFDTEQKYHGFSKRAYCFMVPEDAPVFEVDGVRIDI--R 336
Db 231 ----HTRR-----EDK-HMF-----FEFPQPLPVC--GDIKVEFFHK 260
Qy 337 EIGFLKKFSKGKIGHWENTMP 358
Db 261 QNKMLKK---DKMFHFWNTFF 279

RESULT 3
O54857
ID O54857 PRELIMINARY; PRT; 403 AA.
AC O54857;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein tyrosine phosphatase and tensin homolog/mutated in multiple
DE advanced cancers protein.
GN PTEN/MMAC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Roz L., Finocchiaro G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017185; AAB96620.1; --
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 47118 MW; 243BFE35FE209FE5 CRC64;

Query Match 9.5%; Score 491.5; DB 11; Length 403;
Best Local Similarity 31.3%; Pred. No. 3.8e-26;
Matches 123; Conservative 57; Mismatches 128; Indels 85; Gaps 12;

Qy 48 IPTAVSSNRCTEYQNIDLCAYITDRIIAGYPAIGATGEANFRNSKVQTOQLTRHGK 107
Db 4 IIKEIVSRNKRYQEDGFDLDTIYNPIIANGFPAERLEGVYRNNDVVRFLDSKH-K 62
Qy 108 GNVKVFNLRGYYVDADNFDGNCVICFDMTDHPPSLELMAPFCREKLEWLEADDKHVI 167
Db 63 NHYKYNLCARHYDTAKENCRVAQYPEDHNPQQLKPKFCEDLDQWLSDDNHVAI 122
Qy 168 HCKAGKRTGVMICALLIYINFPSPQILDYYSIIRTKNNKGVTPSORRYIYYHKLR 227
Db 123 HCKAGKRTGVMICAYLLHGRGFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYSVLL 182
Qy 228 BRELNVPLRMQLIGVYVERPPKTWGGG-----KIKVEVNG-GSTILFKPDPLII 277
Db 183 KNHLDYRPVALLFHKKMFETIPMFSGGTGTCNPQPVVYQLKVKIYSSNGPT----- 232
Qy 278 KSNHQRERATWLNCDTNEFDTEQKYHGFSKRAYCFMVPEDAPVFEVDGVRIDI-- 335
Db 233 -----RRE-----DKLMY-FEFPQPLPVC--GDIKVEFFH 259
Qy 336 REIGFLKKFSKGKIGHWENTMP-----ACDGLNG-GHFEYVDKTPQYI 379
Db 260 QNKMLKK---DKMFHFWNTFFIPGPBETSEKVENGLCDQEIISIERADNDKEYL 316
Qy 380 GDDTSIGRKGMRNETPMRKIDPETGNEFESP 412
Db 317 -----VLTLTKNLDLKDANKKANKRYFSP 339

RESULT 4
O43460
ID O43460 PRELIMINARY; PRT; 403 AA.
AC O43460;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog 2 (Fragment).
GN PTH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC MEDLINE=98127441; PubMed=9467947;
RA Kim S.K., Su L.K., Oh Y., Kemp B.L., Hong W.K., Mao L.;
RT "Alterations of PTEN/MMAC1, a candidate tumor suppressor gene, and its
RT homologue, PTH2, in small cell lung cancer cell lines.";
RL Oncogene 16:89-93(1998).
DR EMBL; AF019083; AAC52017.1; --
DR Genew; HGNC:9589; PTENP1.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 403 AA; 47163 MW; BDD42A4D0F26B419 CRC64;

Query Match 9.2%; Score 474.5; DB 4; Length 403;
Best Local Similarity 30.1%; Pred. No. 5.9e-25;
Matches 118; Conservative 57; Mismatches 134; Indels 83; Gaps 11;

Qy 48 IPTAVSSNRCTEYQNIDLCAYITDRIIAGYPAIGATGEANFRNSKVQTOQLTRHGK 107
Db 4 IIKEIVSRNKRYQEDGFDLDTIYNPIIANGFPAERLEGVYRNNDVVRFLDSKH-K 62
Qy 108 GNVKVFNLRGYYVDADNFDGNCVICFDMTDHPPSLELMAPFCREKLEWLEADDKHVI 167
Db 63 NHYKYNLCARHYDTAKSNRYVAQYPEDHNPQQLKPKFCEDLDQWLSDDNHVAI 122
Qy 168 HCKAGKRTGVMICALLIYINFPSPQILDYYSIIRTKNNKGVTPSORRYIYYHKLR 227
Db 123 HCKAGKRTGVMICAYLLHGRGFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYSVLL 182
Qy 228 BRELNVPLRMQLIGVYVERPPKTWGGG-----KIKVEVNGSTILFKPDPLII 278
Db 183 KNHLDYRPVALLFHKKMFETIPMFSGGTGTCNPQPVVYQLKVKIYSSNGP----- 231
Qy 279 KSNHQRERATWLNCDTNEFDTEQKYHGFSKRAYCFMVPEDAPVFEVDGVRIDI--R 336
Db 232 -----TRW-----EDKF-----MYFEFPQPLPVC--GDIKVEFFHK 260
Qy 337 EIGFLKKFSKGKIGHWENTMP-----ACDGLNG-GHFEYVDKTPQYI 380
Db 261 QNKMLKK---DKMFHFWNTFFIPGPBETSEKVENGLCDQEIISIERADNDKEYL- 316
Qy 381 DDTSIGRKGMRNETPMRKIDPETGNEFESP 412
Db 317 -----VLTLTKNLDLKDANKKANKRYFSP 339

RESULT 5
O14781
ID O14781 PRELIMINARY; PRT; 338 AA.
AC O14781;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN PTEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```



```
QY 546 GNLAHNESTRRLQALTONMFKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKNG--ACSE 603
Db 443 RNHIFNQPSIKKTDLI-----KW-----QNSEVHITRSINENKNI-NYNSYITCKQ 487
QY 604 N 604
Db 488 S 488

RESULT 10
QYOB5
ID QYOB5 PRELIMINARY; PRT; 511 AA.
AC QYOB5; Q9U469;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE PTEN protein (EC 3.1.3.48) (Phosphatase and tensin homolog).
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith A.;
RT "Alternative splicing of the Drosophila PTEN Gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 100-511 FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE=20085000; PubMed=10617573;
RA Gberdhan D.C.I., Patricio N., Goodman E.C., Mlodzik M., Wilson C.;
RT "Drosophila tumor suppressor PTEN controls cell size and number by
RT antagonising the Chico/PI3-kinase signaling pathway.";
RL Genes Dev. 13:3244-3258(1999).
DR EMBL; AF161258; AAD45363.1; -.
DR EMBL; AF201906; AAF23237.1; -.
DR FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR PHOSPHATASE_2; 1.
KW Alternative splicing; Hydrolase.
SQ SEQUENCE 511 AA; 58650 MW; 10AB4A19D3DC04D5 CRC64;

Query Match 8.5%; Score 441.5; DB 5; Length 511;
Best Local Similarity 26.3%; Pred. No. 1.7e-22;
Matches 158; Conservative 82; Mismatches 206; Indels 155; Gaps 27;

QY 42 VERIRHIFRTAVSSNRCTEYQNIDLCAYITDRIAGYPATG-IEANFRNSKVQTOQF 100
Db 5 ISLMNVRNVSKRIYKERYGDLDTYINDNIAMGYAPADPKLEGLFRNRLEDVFKL 64
QY 101 LTRFRHGKGNVFNLRGGVYVDADNFDGNVICFDMTDHHPSPLELMAPCREAKEWLEAD 160
Db 65 LEENHAQ-HYKINLCERSYDVAKRGKRVAVPPDDHNPPTIELIQPCSDVDMWLKED 123
QY 161 DRKHVAVHCKAGRTGVMICALLIYINFPSPRQILDYYSIIRTKNNKGVITPSQRRYI 220
Db 124 SSVNVAHVCKAGRTGVMICAYLVFSGIKSADEALAWYDEKRTKDRKGVITPSQRRYV 183
QY 221 YYHKL-----RRELNYLPLR-----MQLIGYVVERPKTWGGSGKIKVEVNGNST 267
Db 184 QYFSLVCSVPYSKSVSLNVCIRFSESSCVQLGM-VE-----CSISV-LHDSAT 232
QY 268 ILFKPDELIIKSNHQRATWLNCCDTPNEFDTEQKYHGVFSKRAVCFMVPEDAPVFV 327
Db 233 ENAKPDLR-----KTUFDIF-----QKSFVLTIKPSIP--V 261
```

```
QY 328 EGDVRIDIREIGFLKPSDGGKIGHWFWNTMFA-----CDGGLNGGHFEYVDKTOPYIG 380
Db 262 SGDVKFEL-----TKKSPDKIICHFWLNTFFVRNYSPOCESDGTVN-----KYHTLSKSEI 312
QY 381 DDTSIGRKNRMNETPMRKIDP--ETGNFEFSPQIUNPPGLEKHITTEQAMENYNY- 437
Db 313 DDV---HKDSEHKRFSSEFKISIVFEAEY-FSN-----DVQAEASEKERNENVLNFE 360
QY 438 -----GMIPPRYTISKILHEKHEGIVKDDYNDRLKPLMGDKSYTESGSGDINGVGGPPE 492
Db 361 RSDYDSLSPNCYAEKVL-----TAIVNDNTT-----KSQT----- 391
QY 493 IPIYAEHVLTFPVYEMDRALKSKDLNMGKMLHVLRVCDTRDSKWM-----EKSEVF 545
Db 392 --IETLDHKDIIVTKIYDVTSTNSKNTSTACR-----KQPNSTKTLPLSLNDSTKEIK 442
QY 546 GNLAHNESTRRLQALTONMFKWRPEPCAFSGKGAEMHYPPSVRYSSNDGKNG--ACSE 603
Db 443 RNHIFNQPSIKKTDLI-----KW-----QNSEVHITRSINENKNI-NYNSYITCKQ 487
QY 604 N 604
Db 488 S 488

RESULT 11
QYH106
ID QYH106 PRELIMINARY; PRT; 632 AA.
AC QYH106;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative tyrosine phosphatase.
GN ATG50110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT000931; AAN41331.1; -.
SQ SEQUENCE 632 AA; 70072 MW; B1BDD935DD63083F CRC64;

Query Match 8.5%; Score 438; DB 10; Length 632;
Best Local Similarity 25.5%; Pred. No. 4.1e-22;
Matches 157; Conservative 79; Mismatches 195; Indels 184; Gaps 26;

QY 3 TPDPDVSTSTRSMARDL---QENPNR-----QPGEPVRS 34
Db 91 SPPSFSSGLSSWAKSKFKQQDPNRTDSCMSAFRTSELGLHLPTKGSEVGDSSRS 150
QY 35 -----EPYHNSIVE-----RIRHIFTAVSSNRCTEYQNIDLCAYITDR 75
Db 151 NTQVGAPESLTKAVDSSRGAVKAMQVKARHI-----VQNKRRYQEGEFDLDMTYTEN 206
QY 76 IATGYPATGI-----EAFNRNSKVQTOQLTRRHGKGNVFNLRGGVYVDADNFD 127
Db 207 IIAAGFPAGDITSSGLFGFEGLYRNHMEVTKFFETHH-KDKYKVINLCSERLDASRFE 265
QY 128 GNVICFDMTDHHPSPLELMAPCREAKEWLEADKHVAVHCKAGRTGVMICALLIYI 187
Db 266 GKVASFPDDHNCPIQLIPSCQSAYTWLKEDIQNVVVHCKAGMARTGLMICLLLYL 325
QY 188 NFYSPRQILDYYSIIRTKNNKGVITPSQRRYIYYHYHKLREELNYLP--LRMQLIGV-- 243
```

```

Db 326 KFFPTAEBAIDYNNQKRLDGLKALVLPQIRVYKYYVQNFQDGKVPERRCMLRGLPRL 385
Qy 244 ----YVERPPTWGGGSKIKVEVNGSTILFKPDPDLIISKSHQERATWLNCDTPNEF 299
Db 386 INCPYWRP-----AITISNHTDILF-----STKKHOKTK----- 415
Qy 300 DTGEQYHGFVSKR-AYCFMWPEDAPVF-VEGDVRIDIREIGFLKFKSGKIGHVFNFTM 357
Db 416 DLGPEDFWTKAPKKGVVFAIPEAGLTLAGDFKIHQD-----SDGDF-YCWLNTT 467
Qy 358 FA-----CDG-----GLNGGHFEYV-----DKTQP-----YIGDDTSIGRK 388
Db 468 LTNRTMLKSGDFDGFDRKRLPAPGFHVEIVMEPDNSQPTKSKSDSTQQSQSSADS 527
Qy 389 NGMRRNETPMRKIDPETGNEFESPMQIVNPPGLEKHITTEQAMENYVGMTPPYRTISK 448
Db 528 SKLKSNEKDDDDVFSDDGEE-----EGNSQSYSTNEKTASSMHTTSK 569
Qy 449 ILHEKHEKGIKDDYNDRLKPMGDKSYTESGKSG-----DIRGVGGPFEIPY 495
Db 570 -PHQINEPP-KRDD-----PSANKSVTSSSGHYNPNNLSLAVSDIKATA----- 614
Qy 496 KAEHVLTPPVYEMD 510
Db 615 -ADASVFSFGDEED 628

RESULT 12
Q9SN07 PRELIMINARY; PRT; 628 AA.
AC Q9SN07;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative tyrosine phosphatase.
GN F3A4.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eumids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Barges M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Newes H.W., Lemcke K., Mayer K.F.X., Quekier F., Salanoubat M.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI32978; CAB62119.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 628 AA; 69569 MW; DF8AC76D03D7B8CC CRC64;

Query Match 8.5%; Score 437; DB 10; Length 628;
Best Local Similarity 25.5%; Pred. No. 4.8e-22;
Matches 156; Conservative 80; Mismatches 195; Indels 180; Gaps 26;

Qy 3 TPPDPVSTSTSMARDL---QENPNR-----RIHFTAVSSNRCRTEYQNIIDLCAVITDR 75
Db 91 SPFSIFSSGLSSWAKSPKFQQQDPNRTDSGMSAFRTFSLGLHLPTKSGSEVGDSRSS 150
Qy 35 -----EPYHNSIVE-----VSQNRKRRVQEGFDDMTYIEN 206
Db 151 NTQVGAFPSLTAKVDSRGAQKAMQVKAHI-----VSQNRKRRVQEGFDDMTYIEN 206
Qy 76 IIAIGYPATGI-----EAFNRKSVQTOQFLTRRHGKGNVKNVFNLRGGYVADNPD 127
Db 207 IIAAGFPAGDISGLFGFEGLYRNHMEVIRFFETH-KDKYKVNLCSERLYDASRPE 265

```

```

Qy 128 GNVICFDMTHHPPSLELMAPFCREAKEWLEADKKHVIATVHCAGKAGRTGVMICALLIYI 187
Db 266 GKVASFPDDNCPPIQIPSCASAYTWLKEDQNVVVHCAGMARTGLMICCLLYL 325
Qy 188 NFYSPRQLDYGIITKNNKGVITPSQRYIYYHKLREELNPLR---MQLIGV- 243
Db 326 KFFPTAEBAIDYNNQKRLDGLKALVLPQIRVYKYYVQNFQDGKVPERRCMLRGLPRL 385
Qy 244 YVERPPTWGGGSKIKVEVNGSTILFKPDPDLIISKSHQERATWLNCDTPNEFDTGE 303
Db 386 YWRP-----AITISNHTDILF-----STKKHOKTK-----DLGP 415
Qy 304 QYHGFVSKR-AYCFMWPEDAPVF-VEGDVRIDIREIGFLKFKSGKIGHVFNFTMFA-- 359
Db 416 EDFWIKAPKKGVVFAIPEAGLTLAGDFKIHQD-----SDGDF-YCWLNTTLDN 467
Qy 360 -----CDG-----GLNGGHFEYV-----DKTQP-----YIGDDTSIGRKNGMR 392
Db 468 RTMLKSGDFDGFDRKRLPAPGFHVEIVMEPDNSQPTKSKSDSTQQSQSSADS 527
Qy 393 RNETPMRKIDPETGNEFESPMQIVNPPGLEKHITTEQAMENYVGMTPPYRTISKILHE 452
Db 528 SNEKDDDDVFSDDGEE-----EGNSQSYSTNEKTASSMHTTSK-PHQ 568
Qy 453 KHEKGIKDDYNDRLKPMGDKSYTESGKSG-----DIRGVGGPFEIPYKAE 499
Db 569 INEPP-KRDD-----PSANKSVTSSSGHYNPNNLSLAVSDIKATA-----ADA 613
Qy 500 HVLTPPVYEMD 510
Db 614 SVFSFGDEED 624

RESULT 13
Q9Y0B6 PRELIMINARY; PRT; 418 AA.
AC Q9Y0B6;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE PTEN1 (EC 3.1.3.48) (CG5671-PC).
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith A.;
RA "Alternative splicing of the Drosophila PTEN Gene.";
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
EX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brackley P., Brattier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

```



```

Db 182 IRESIKYVPRNTLTKKIVLRPLPKELNLSVGNKCVFNSKEHNMVVISKKKT 241
Qy 276 IISK-----SNHQRERATWL-----NN 292
Db 242 VVDKNKDPKKLTKENSEKNIDSSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 301
Qy 293 CDTPN-----EFD-----TGEQKYHGFVSKRAYCFMVPEAPVFEVDVRI 333
Db 302 VGTVNGNTLHQLGGSQFSLDLADGNTIGNDEYISF-----EIGALSLAGDIRI 350
Qy 334 DIREIGFLKFKDGKIGHVWNTMFACD-----GGLNGGHFEYVDKTPQYIGDD---T 383
Db 351 E-----FTNK-QDDRMFMFWNTSFVQOLEIIPKSGLDKAH---KDKNHKAFPEHFVEL 401
Qy 384 SIGRKNMGRRNETPMRKIDPETGNE 408
Db 402 TFDQLDQQQSHTTVVASAEQTNNQ 426

```

RESULT 15

```

Q8T9S7
ID Q8T9S7 PRELIMINARY; PRT; 533 AA.
AC Q8T9S7;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Pten 3-phosphoinositide phosphatase alpha.
GN PTENA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44889;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ax3;
RA Meili R., Firtel R.A.;
RT "Spatial and temporal regulation of Dictyostelium discoideum chemotaxis by PTEN.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467431; AAL75566.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE.1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 533 AA; 59831 MW; 9922F7887D6F9F6A CRC64;

```

```

Query Match 8.3%; Score 431; DB 5; Length 533;
Best Local Similarity 26.3%; Pred. No. 9.9e-22;
Matches 117; Conservative 68; Mismatches 156; Indels 104; Gaps 13;
Qy 47 HIFRTAVSNRCRTEYQNIIDLCAYITDRIIAGYDPATGIEANFRNSKVQTOQFLTRRHG 106
Db 3 NLLRVAVSQKRYQKNGYDLDLAYITDNIIVAMGPFSEKVEGFRNPMKDVQRFDDQVH- 61
Qy 107 KGNVKVFNLRGGYYVDADNFDGNCVCFDMDTHPPSLPELMAPCEKAEKLEADDKHVIA 166
Db 62 KDHFKNVNLCSERVYDHSKPYGRVGYPPDFDHNAPQFEMIDAFCDVDADWAKEDSKNTAV 121
Qy 167 VHCKAGKGRGTGMICALLIYINFPSPROIIDYISIRTKNKGVTIPSQRRYIYYHKL 226
Db 122 IHCKAGKGRGTGLMICCWLAYCGWKNTEDSLRFAALRTYNQKVTIPSQIRYVGYFGS 181
Qy 227 RERELNPLRMQLIGVYVERPPKTWG-GGSKIKEVG-----NGSTILFKPDPL 275
Db 182 IRESIKYVPRNTLTKKIVLRPLPKELNLSVGNKCVFNSKEHNMVVISKKKT 241
Qy 276 IISK-----SNHQRERATWL-----NN 292
Db 242 VVDKNKDPKKLTKENSEKNIDSSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 301
Qy 293 CDTPN-----EFD-----TGEQKYHGFVSKRAYCFMVPEAPVFEVDVRI 333
Db 302 VGTVNGNTLHQLGGSQFSLDLADGNTIGNDEYISF-----EIGALSLAGDIRI 350

```

```

Qy 334 DIREIGFLKFKDGKIGHVWNTMFACD-----GGLNGGHFEYVDKTPQYIGDD---T 383
Db 351 E-----FTNK-QDDRMFMFWNTSFVQOLEIIPKSGLDKAH---KDKNHKAFPEHFVEL 401
Qy 384 SIGRKNMGRRNETPMRKIDPETGNE 408
Db 402 TFDQLDQQQSHTTVVASAEQTNNQ 426

```

Search completed: December 10, 2003, 20:34:13
Job time : 56.8125 secs